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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 67.6736 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202

Perfect score: 1032

Sequence: 1 HPELVVKVKAEDQLGARVG.....IDMWEADKAVGPLRLSALPA 202

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	263	15	US-10-668-778-2
2	1032	100.0	286	10	US-09-919-901-7
3	1032	100.0	286	10	US-09-919-901-14
4	1032	100.0	286	10	US-09-919-901-21
5	1032	100.0	286	11	US-09-837-306-354
6	1032	100.0	286	14	US-10-191-966-7
7	1032	100.0	286	14	US-10-191-966-14
8	1032	100.0	286	15	US-10-191-966-21
9	1032	100.0	286	15	US-10-045-674-523
10	1032	100.0	286	16	US-10-416-708A-73
11	1032	100.0	2307	10	US-09-919-901-2

ALIGNMENTS

12	1032	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	1032	100.0	2307	10	US-09-919-901-16	Sequence 16, Appli
14	1032	100.0	2307	14	US-10-191-966-2	Sequence 2, Appli
15	1032	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	1032	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	1031	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	1031	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
19	1031	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	1031	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	1027	99.5	265	9	US-09-772-114-6	Sequence 6, Appli
22	1027	99.5	265	14	US-10-280-482-2	Sequence 2, Appli
23	1027	99.5	265	17	US-10-656-029-2	Sequence 2, Appli
24	1027	99.5	285	9	US-09-772-114-7	Sequence 7, Appli
25	1027	99.5	286	14	US-10-016-668-5	Sequence 5, Appli
26	1027	99.5	286	14	US-10-280-482-4	Sequence 4, Appli
27	1027	99.5	286	17	US-10-656-029-4	Sequence 4, Appli
28	1027	99.5	286	17	US-10-877-952-26	Sequence 26, Appli
29	1027	99.5	286	17	US-10-877-952-71	Sequence 71, Appli
30	1024	99.2	264	17	US-10-877-952-18	Sequence 18, Appli
31	1024	99.2	362	15	US-10-469-199-2	Sequence 2, Appli
32	1024	99.2	584	9	US-10-890-675-2	Sequence 2, Appli
33	1020	98.8	265	9	US-09-772-114-8	Sequence 8, Appli
34	1020	98.8	265	14	US-10-280-482-6	Sequence 6, Appli
35	1020	98.8	265	16	US-10-622-088-114	Sequence 114, App
36	1020	98.8	265	17	US-10-656-029-6	Sequence 6, Appli
37	1020	98.8	265	17	US-10-877-952-154	Sequence 154, App
38	1019	98.7	264	9	US-09-772-114-9	Sequence 9, Appli
39	1019	98.7	264	14	US-10-280-482-8	Sequence 8, Appli
40	1019	98.7	264	17	US-10-656-029-8	Sequence 8, Appli
41	1012.5	98.1	262	14	US-10-177-725-3	Sequence 3, Appli
42	1012.5	98.1	262	15	US-10-393-449-3	Sequence 3, Appli
43	1004	97.3	498	17	US-10-491-653-146	Sequence 146, App
44	993	96.2	284	15	US-10-052-188-2	Sequence 2, Appli
45	463	44.9	94	9	US-09-925-258-760	Sequence 760, App

RESULT 1

US-10-668-778-2

Sequence 2, Application US/10668778

Publication No. US2004003817A1

GENERAL INFORMATION:

APPLICANT: Ballint, Robert F.

APPLICANT: Kalobios, Inc.

TITLE OF INVENTION: Interaction-Activated Proteins

FILE REFERENCE: 021167-000700US

CURRENT APPLICATION NUMBER: US/10/668, 778

PRIOR FILING DATE: 2003-09-22

PRIOR APPLICATION NUMBER: US/09/526, 106

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-03-15

PRIOR APPLICATION NUMBER: US 60/135,926

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 60/175,968

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 263

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:

OTHER INFORMATION: TEM-1 beta-lactamase

US-10-668-778-2

Query Match 100.0%; Score 1032; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.

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Query Match      100.0%; Score 103; DB 10; Length 286;
Best Local Similarity 100.0%; Prod. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 HPELVKVAEDDGLGARVGTEELDLSKTLSEFRPEERPPMNSTFNTLLCGAVLSRID 60
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Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGOEOLGRRIRHSQNDLVESPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGSP 120
Db 84 AGOEOLGRRIRHSQNDLVESPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRWPEBELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KELTAFILNMGDHYRLDRWPEBELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QLIDWMEADKVGAPLLRSALPA 202
Db 204 QLIDWMEADKVGAPLLRSALPA 225

RESULT 5
US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: PCBS5
US-09-837-306-354

Query Match 100.0%; Score 1032; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGOEOLGRRIRHSQNDLVESPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGSP 120
Db 84 AGOEOLGRRIRHSQNDLVESPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRWPEBELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KELTAFILNMGDHYRLDRWPEBELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QLIDWMEADKVGAPLLRSALPA 202
Db 204 QLIDWMEADKVGAPLLRSALPA 225

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1032; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
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Qy 61 AGOEOLGRRIRHSQNDLVESPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGSP 120
Db 84 AGOEOLGRRIRHSQNDLVESPTVEKHLTDGMTVRELCSAATMSDNTANLLTTIGSP 143
Qy 121 KELTAFILNMGDHYRLDRWPEBELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KELTAFILNMGDHYRLDRWPEBELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QLIDWMEADKVGAPLLRSALPA 202
Db 204 QLIDWMEADKVGAPLLRSALPA 225

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 1032; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KELTAPFLHMGDHYTRLDRMEPELNEALPNDERDITPMVAMATTLTKLLTSELTLASRQ 180
DB 144 KELTAPFLHMGDHYTRLDRMEPELNEALPNDERDITPMVAMATTLTKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRLSALPA 202
DB 204 QLIDMMEADKVAAGPLRLSALPA 225

RESULT 8
US-10-191-966-21

Sequence 21, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Poter, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 1032; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGARVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGARVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KELTAPFLHMGDHYTRLDRMEPELNEALPNDERDITPMVAMATTLTKLLTSELTLASRQ 180
DB 144 KELTAPFLHMGDHYTRLDRMEPELNEALPNDERDITPMVAMATTLTKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRLSALPA 202
DB 204 QLIDMMEADKVAAGPLRLSALPA 225

RESULT 9
US-10-045-674-523

Sequence 523, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DVA/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match 100.0%; Score 1032; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGARVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGARVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KELTAPFLHMGDHYTRLDRMEPELNEALPNDERDITPMVAMATTLTKLLTSELTLASRQ 180
DB 144 KELTAPFLHMGDHYTRLDRMEPELNEALPNDERDITPMVAMATTLTKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRLSALPA 202
DB 204 QLIDMMEADKVAAGPLRLSALPA 225

RESULT 10
US-10-416-708A-73

Sequence 73, Application US/10416708A
Publication No. US20040161753A1
GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Kacja
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 73
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 1032; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGARVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGARVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 83

QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRMBEDELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRMBEDELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 203
QY 181 OLIDWMEADKVAAGPLRSALPA 202
DB 204 OLIDWMEADKVAAGPLRSALPA 225

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 1032; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADDOUGARVGYIELDNGSKILSPRPERPMMSTFKVLLCGAVLSRID 60
DB 2045 HPELVKVKDADDOUGARVGYIELDNGSKILSPRPERPMMSTFKVLLCGAVLSRID 2104
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 120
DB 2105 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 2164
QY 121 KELTAFILNMGDHVTRLDRMBEDELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 180
DB 2165 KELTAFILNMGDHVTRLDRMBEDELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 2224
QY 181 OLIDWMEADKVAAGPLRSALPA 202
DB 2225 OLIDWMEADKVAAGPLRSALPA 2246

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 1032; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADDOUGARVGYIELDNGSKILSPRPERPMMSTFKVLLCGAVLSRID 60
DB 2045 HPELVKVKDADDOUGARVGYIELDNGSKILSPRPERPMMSTFKVLLCGAVLSRID 2104
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 120
DB 2105 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 2164
QY 121 KELTAFILNMGDHVTRLDRMBEDELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 180
DB 2165 KELTAFILNMGDHVTRLDRMBEDELNEAIPNDRDITMPVAMATTIRKLLTGELITLASRQ 2224
QY 181 OLIDWMEADKVAAGPLRSALPA 202
DB 2225 OLIDWMEADKVAAGPLRSALPA 2246

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 1032; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADDOUGARVGYIELDNGSKILSPRPERPMMSTFKVLLCGAVLSRID 60
DB 2045 HPELVKVKDADDOUGARVGYIELDNGSKILSPRPERPMMSTFKVLLCGAVLSRID 2104
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 120

Db 2105 AGOQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QIIMWEADKVAAGPLRSALPA 202
Db 2225 QIIMWEADKVAAGPLRSALPA 2246

RESULT 14
US-10-191-966-2
Sequence 2, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Poters, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 1032; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AGOQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
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Db 2165 KETAFIHNMGDHYTRLDRWPEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QIIMWEADKVAAGPLRSALPA 202
Db 2225 QIIMWEADKVAAGPLRSALPA 2246

RESULT 15
US-10-191-966-9
Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Poters, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 1032; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-98;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AGOQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
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Db 2225 QIIMWEADKVAAGPLRSALPA 2246

Search completed: June 10, 2005, 11:09:06
Job time : 67.6736 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 63.6534 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975

Sequence: 1 HPELVKVKADBDQIGARVG.....GELTLASRQQLDWWEADK 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	263	US-10-668-778-2	Sequence 2, Appli
2	975	100.0	286	US-09-919-901-7	Sequence 7, Appli
3	975	100.0	286	US-09-919-901-14	Sequence 14, Appli
4	975	100.0	286	US-09-919-901-21	Sequence 21, Appli
5	975	100.0	286	US-09-837-306-354	Sequence 354, App
6	975	100.0	286	US-10-191-966-7	Sequence 7, Appli
7	975	100.0	286	US-10-191-966-14	Sequence 14, Appli
8	975	100.0	286	US-10-191-966-21	Sequence 21, Appli
9	975	100.0	286	US-10-045-674-523	Sequence 523, App
10	975	100.0	286	US-10-416-708A-73	Sequence 73, Appli
11	975	100.0	2307	US-09-919-901-2	Sequence 2, Appli

12	975	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	975	100.0	2307	14	US-09-919-901-16	Sequence 16, Appli
14	975	100.0	2307	10	US-10-191-966-2	Sequence 2, Appli
15	975	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	975	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	974	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	974	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
19	974	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	974	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	970	99.5	265	9	US-09-772-114-6	Sequence 6, Appli
22	970	99.5	265	14	US-10-280-482-2	Sequence 2, Appli
23	970	99.5	265	17	US-10-656-029-2	Sequence 2, Appli
24	970	99.5	285	9	US-09-772-114-7	Sequence 7, Appli
25	970	99.5	286	14	US-10-016-668-5	Sequence 4, Appli
26	970	99.5	286	14	US-10-280-482-4	Sequence 4, Appli
27	970	99.5	286	17	US-10-656-029-4	Sequence 4, Appli
28	970	99.5	286	17	US-10-877-952-26	Sequence 26, Appli
29	970	99.5	286	17	US-10-877-952-71	Sequence 71, Appli
30	967	99.2	264	17	US-10-877-952-18	Sequence 18, Appli
31	967	99.2	362	15	US-10-469-199-2	Sequence 2, Appli
32	967	99.2	584	17	US-10-890-675-2	Sequence 2, Appli
33	963	98.8	265	9	US-09-772-114-8	Sequence 8, Appli
34	963	98.8	265	14	US-10-280-482-6	Sequence 6, Appli
35	963	98.8	265	16	US-10-622-088-114	Sequence 114, App
36	963	98.8	265	17	US-10-656-029-6	Sequence 6, Appli
37	963	98.8	265	17	US-10-877-952-154	Sequence 154, App
38	962	98.7	264	9	US-09-772-114-9	Sequence 9, Appli
39	962	98.7	264	14	US-10-280-482-8	Sequence 8, Appli
40	962	98.7	264	17	US-10-656-029-8	Sequence 8, Appli
41	955.5	98.0	262	14	US-10-177-725-3	Sequence 3, Appli
42	955.5	98.0	262	15	US-10-393-449-3	Sequence 3, Appli
43	947	97.1	498	17	US-10-491-653-146	Sequence 146, App
44	936	96.0	284	15	US-10-062-188-2	Sequence 2, Appli
45	463	47.5	94	9	US-09-925-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US20040038317A1
GENERAL INFORMATION:
APPLICANT: Ballint, Robert F.
APPLICANT: Her, Jeng-Hong
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%; Score 975; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 9e-95;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITTMVAMATTIRKLLTGELLTLASRQ 180
QY 181 QLIDMMEADK 190
Db 181 QLIDMMEADK 190
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RESULT 2

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US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-7
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Query Match 100.0%; Score 975; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 24 HPEITLVKVKDAEDQUGARVGYIELDLSNGKILIESFRPERPFPMSSTFKVLLCGAVLSRID 83
QY 61 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATYMSDNTAANLLTTIGSP 120
Db 84 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATYMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITTMVAMATTIRKLLTGELLTLASRQ 180
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QY 181 QLIDMMEADK 190
Db 204 QLIDMMEADK 213
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RESULT 3

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US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
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; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-14
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Query Match 100.0%; Score 975; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 24 HPEITLVKVKDAEDQUGARVGYIELDLSNGKILIESFRPERPFPMSSTFKVLLCGAVLSRID 83
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Db 84 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATYMSDNTAANLLTTIGSP 143
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Db 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDITTMVAMATTIRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
Db 204 QLIDMMEADK 213
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RESULT 4

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US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION:
US-09-919-901-21
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Query Match 100.0%; Score 975; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 204 QUIDMWEADK 213

RESULT 5

US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOEF, RENE

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
FILE REFERENCE: DYAK/002
CURRENT APPLICATION NUMBER: US/09/837,306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 354
LENGTH: 286
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:

OTHER INFORMATION: Description of Unknown Organism: PCBS5
US-09-837-306-354

Query Match 100.0%; Score 975; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPEERPFMMSTFKVLLCGAVLSRID 83
Qy 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHVRRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGSELTLASRQ 180
Db 144 KELTAFILNMGDHVRRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGSELTLASRQ 203
Qy 181 QUIDMWEADK 190
Db 204 QUIDMWEADK 213

RESULT 6

US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:

APPLICANT: Potts, Karen E.
APPLICANT: JACKSON, ROBERTA L.
APPLICANT: PATICK, AMY K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 975; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPEERPFMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPEERPFMMSTFKVLLCGAVLSRID 83
Qy 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
Qy 121 KELTAFILNMGDHVRRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGSELTLASRQ 180
Db 144 KELTAFILNMGDHVRRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGSELTLASRQ 203
Qy 181 QUIDMWEADK 190
Db 204 QUIDMWEADK 213

RESULT 7

US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:

APPLICANT: Potts, Karen E.
APPLICANT: JACKSON, ROBERTA L.
APPLICANT: PATICK, AMY K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :

US-10-191-966-14

Query Match 100.0%; Score 975; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPEERPFMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGRVGYIELDLSGKILSFRRPEERPFMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRRHYHSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOELGRRHYHSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 OLIDMMEADK 190
DB 204 OLIDMMEADK 213

RESULT 8
US-10-191-966-21

Sequence 21, Application US/10191966
Publication No. US20030175692A1

GENERAL INFORMATION:

APPLICANT: Potes, Karen E.
APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT FILING DATE: 2002-07-10

PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: :

US-10-191-966-21

Query Match 100.0%; Score 975; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQAGAVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDABDQAGAVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGOELGRRHYHSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOELGRRHYHSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 OLIDMMEADK 190
DB 204 OLIDMMEADK 213

RESULT 9
US-10-045-674-523

Sequence 523, Application US/10045674
Publication No. US2003023233A1

GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.

APPLICANT: COHEN, EDWARD H.

APPLICANT: NASTRI, HORACIO G.

APPLICANT: ROONEY, KRISTIN L.

APPLICANT: HOET, RENE

APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.

;; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
;; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
;; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
;; TITLE OF INVENTION: LIBRARIES
;; FILE REFERENCE: DXX/002 CIP2
;; CURRENT APPLICATION NUMBER: US/10/045,674
;; PRIOR FILING DATE: 2001-10-25
;; PRIOR APPLICATION NUMBER: 60/198,069
;; PRIOR FILING DATE: 2000-04-17
;; PRIOR APPLICATION NUMBER: 09/837,306
;; PRIOR FILING DATE: 2001-04-17
;; NUMBER OF SEQ ID NOS: 635
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 523
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match 100.0%; Score 975; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQAGAVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDABDQAGAVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGOELGRRHYHSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOELGRRHYHSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWPEBELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 OLIDMMEADK 190
DB 204 OLIDMMEADK 213

RESULT 10
US-10-416-708A-73

Sequence 73, Application US/10416708A
Publication No. US20040161753A1

GENERAL INFORMATION:

APPLICANT: Wise, John G.

APPLICANT: Fromknecht, Katja

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING

FILE REFERENCE: 3779-0004

CURRENT APPLICATION NUMBER: US/10/416,708A

PRIOR FILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.2

SEQ ID NO 73

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Construct

US-10-416-708A-73

Query Match 100.0%; Score 975; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQAGAVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDABDQAGAVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 83

Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 120
Db 84 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 143
Qy 121 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 180
Db 144 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 203
Qy 181 OLIDMEADK 190
Db 204 OLIDMEADK 213

RESULT 11

US-09-919-901-2
Sequence 2, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 975; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKDADQDGAHVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDADQDGAHVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 120
Db 2105 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 2164
Qy 121 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 180
Db 2165 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 2224
Qy 181 OLIDMEADK 190
Db 2225 OLIDMEADK 2234

RESULT 12

US-09-919-901-9
Sequence 9, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901

Qy 121 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 180
Db 144 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 203
Qy 181 OLIDMEADK 190
Db 204 OLIDMEADK 213
Qy 181 OLIDMEADK 190
Db 2225 OLIDMEADK 2234

Query Match 100.0%; Score 975; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKDADQDGAHVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDADQDGAHVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 120
Db 2105 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 2164
Qy 121 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 180
Db 2165 KETLAFILNMGDHTVRLDRWEPELNEALPNDERDTTMAPVAAATTKLLTGELTLASRQ 2224
Qy 181 OLIDMEADK 190
Db 2225 OLIDMEADK 2234

RESULT 13

US-09-919-901-16
Sequence 16, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REFORER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 975; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKDADQDGAHVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDADQDGAHVGYIELDLSNGKILSPRPERPMMSTFKVLLCGAVLSRID 2104
Qy 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTANLLTTIGSP 120

Db 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 2164
QY 121 KETAFALNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADK 190
Db 2225 QLIDWMEADK 2234

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Pottes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 975; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQIGARVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVDABDQIGARVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 2164
QY 121 KETAFALNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADK 190
Db 2225 QLIDWMEADK 2234

RESULT 15
US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Pottes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 975; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQIGARVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVDABDQIGARVGYIEIDLNSGKILSFPRPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 2105 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 2164
QY 121 KETAFALNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALNMGDHVTRLDRWPEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADK 190
Db 2225 QLIDWMEADK 2234

Search completed: June 10, 2005, 11:09:06
Job time : 64.6534 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 60.6383 Seconds

(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925
Sequence: 1 HPELVKVKQADPDQGARVG.....ATTLLKLTGELTLTASRQ 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	925	100.0	263	US-10-668-778-2
2	925	100.0	286	US-09-919-901-7
3	925	100.0	286	US-09-919-901-14
4	925	100.0	286	US-09-919-901-21
5	925	100.0	286	US-09-837-306-354
6	925	100.0	286	US-10-191-966-7
7	925	100.0	286	US-10-191-966-14
8	925	100.0	286	US-10-191-966-21
9	925	100.0	286	US-10-045-674-523
10	925	100.0	286	US-10-416-708A-73
11	925	100.0	2307	US-09-919-901-2

12	925	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	925	100.0	2307	10	US-09-919-901-16	Sequence 16, Appli
14	925	100.0	2307	14	US-10-191-966-2	Sequence 2, Appli
15	925	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	925	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	924	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	924	99.9	286	14	US-10-842-534-9	Sequence 9, Appli
19	924	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	924	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	920	99.5	265	9	US-09-772-114-6	Sequence 6, Appli
22	920	99.5	265	14	US-10-280-482-2	Sequence 2, Appli
23	920	99.5	265	17	US-10-656-029-2	Sequence 2, Appli
24	920	99.5	285	9	US-09-772-114-7	Sequence 7, Appli
25	920	99.5	286	14	US-10-016-668-5	Sequence 5, Appli
26	920	99.5	286	14	US-10-280-482-4	Sequence 4, Appli
27	920	99.5	286	17	US-10-656-029-4	Sequence 4, Appli
28	920	99.5	286	17	US-10-877-952-26	Sequence 26, Appli
29	920	99.5	286	17	US-10-877-952-71	Sequence 71, Appli
30	917	99.1	264	15	US-10-877-952-18	Sequence 18, Appli
31	917	99.1	362	15	US-10-469-199-2	Sequence 2, Appli
32	917	99.1	584	17	US-10-890-675-2	Sequence 2, Appli
33	913	98.7	265	9	US-09-772-114-8	Sequence 8, Appli
34	913	98.7	265	14	US-10-280-482-6	Sequence 6, Appli
35	913	98.7	265	16	US-10-622-088-114	Sequence 114, App
36	913	98.7	265	17	US-10-656-029-6	Sequence 6, Appli
37	913	98.7	265	17	US-10-877-952-154	Sequence 154, App
38	912	98.6	264	9	US-09-772-114-9	Sequence 9, Appli
39	912	98.6	264	14	US-10-280-482-8	Sequence 8, Appli
40	912	98.6	264	17	US-10-656-029-8	Sequence 8, Appli
41	910	98.4	498	17	US-10-491-653-146	Sequence 146, App
42	905.5	97.9	262	14	US-10-177-725-3	Sequence 3, Appli
43	905.5	97.9	262	15	US-10-393-449-3	Sequence 3, Appli
44	886	95.8	284	15	US-10-062-188-2	Sequence 2, Appli
45	463	50.1	94	9	US-09-925-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-10-668-778-2
; Sequence 2, Application US/10668778
; Publication No. US20040038317A1
; GENERAL INFORMATION:
; APPLICANT: Ballint, Robert F.
; APPLICANT: Her, Jeng-Hong
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-000700US
; CURRENT APPLICATION NUMBER: US/10/668, 778
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US/09/526, 106
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124, 339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135, 926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175, 968
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURES:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%; Score 925, DB 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0;

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QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
Db 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
QY 61 AGOQOLGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAITSMDNTAANLLTTIGCP 120
Db 61 AGOQOLGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAITSMDNTAANLLTTIGCP 120
QY 121 KELTAFILNMGDHYTRLDRWPEPELNEAIPNDRDITTMVANAATTLRKLLTGELLTLASRQ 180
Db 121 KELTAFILNMGDHYTRLDRWPEPELNEAIPNDRDITTMVANAATTLRKLLTGELLTLASRQ 180
QY 181 Q 181
Db 181 Q 181

RESULT 2
US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-09-919-901-7

Query Match 100.0%; Score 925; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAITSMDNTAANLLTTIGCP 120
Db 84 AGOQOLGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAITSMDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWPEPELNEAIPNDRDITTMVANAATTLRKLLTGELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRWPEPELNEAIPNDRDITTMVANAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 3
US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
```

```
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-09-919-901-14

Query Match 100.0%; Score 925; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
Db 24 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAITSMDNTAANLLTTIGCP 120
Db 84 AGOQOLGRRHYSONDLYEVSPTVEKHLTDGNTVRELCSAITSMDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWPEPELNEAIPNDRDITTMVANAATTLRKLLTGELLTLASRQ 180
Db 144 KELTAFILNMGDHYTRLDRWPEPELNEAIPNDRDITTMVANAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 4
US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-09-919-901-21

Query Match 100.0%; Score 925; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIETDLSNGKILIESFRPEERPPMSTFVLLCGAVLSRID 60
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Db 24 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATVMSDNTANLLTTIGSP 120
Db 84 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATVMSDNTANLLTTIGSP 143
Qy 121 KELITAFINMGDHYRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGSLLTLASRQ 180
Db 144 KELITAFINMGDHYRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGSLLTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 5
US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837.306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: PCSS5
US-09-837-306-354

Query Match 100.0%; Score 925; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATVMSDNTANLLTTIGSP 120
Db 84 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATVMSDNTANLLTTIGSP 143
Qy 121 KELITAFINMGDHYRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGSLLTLASRQ 180
Db 144 KELITAFINMGDHYRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGSLLTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: JACKSON, ROBERTA L.
; APPLICANT: PATICK, AMY K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 925; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATVMSDNTANLLTTIGSP 120
Db 84 AGQEQGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATVMSDNTANLLTTIGSP 143
Qy 121 KELITAFINMGDHYRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGSLLTLASRQ 180
Db 144 KELITAFINMGDHYRLDRWPELNEAIPNDRDITTMVAMATTIRKLLTGSLLTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: JACKSON, ROBERTA L.
; APPLICANT: PATICK, AMY K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 925; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDABDQAGAVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 120
DB 84 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 143
QY 121 KETLAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 8
US-10-191-966-21

Sequence 21, Application US/10191966
Publication No. US20030175692A1

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08

PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

US-10-191-966-21

Query Match 100.0%; Score 925; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 120
DB 84 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 143
QY 121 KETLAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 9
US-10-045-674-523

Sequence 523, Application US/10045674
Publication No. US2003023233A1

GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.

APPLICANT: COHEN, EDWARD H.

APPLICANT: NASTRI, HORACIO G.

APPLICANT: ROOKEY, KRISTIN L.

APPLICANT: HOET, RENE

APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DVAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Vector pCRESS

US-10-045-674-523

Query Match 100.0%; Score 925; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 120
DB 84 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGP 143
QY 121 KETLAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHVTRLDRWPELNEALPNDERDTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 10
US-10-416-708A-73

Sequence 73, Application US/10416708A
Publication No. US20040161753A1

GENERAL INFORMATION:

APPLICANT: Wise, John G.

APPLICANT: Fromknecht, Katja

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES

FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A

CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.2
SEQ ID NO 73

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Construct

US-10-416-708A-73

Query Match 100.0%; Score 925; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-90;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83

QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
| | | | |
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 143
| | | | |
QY 121 KELTAFILNMGDVTRLDRWPELNEALPNDERTTTPVAMATTIRKLLTGELTLASRQ 180
| | | | |
DB 144 KELTAFILNMGDVTRLDRWPELNEALPNDERTTTPVAMATTIRKLLTGELTLASRQ 203
| | | | |
QY 181 Q 181
| | | | |
DB 204 Q 204
| | | | |

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 925; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKADBDQAGAVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 60
| | | | |
DB 2045 HPEITVKYKADBDQAGAVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 2104
| | | | |
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
| | | | |
DB 2105 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 2164
| | | | |
QY 121 KELTAFILNMGDVTRLDRWPELNEALPNDERTTTPVAMATTIRKLLTGELTLASRQ 180
| | | | |
DB 2165 KELTAFILNMGDVTRLDRWPELNEALPNDERTTTPVAMATTIRKLLTGELTLASRQ 2224
| | | | |
QY 181 Q 181
| | | | |
DB 2225 Q 2225
| | | | |

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 925; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKADBDQAGAVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 60
| | | | |
DB 2045 HPEITVKYKADBDQAGAVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 2104
| | | | |
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
| | | | |
DB 2105 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 2164
| | | | |
QY 121 KELTAFILNMGDVTRLDRWPELNEALPNDERTTTPVAMATTIRKLLTGELTLASRQ 180
| | | | |
DB 2165 KELTAFILNMGDVTRLDRWPELNEALPNDERTTTPVAMATTIRKLLTGELTLASRQ 2224
| | | | |
QY 181 Q 181
| | | | |
DB 2225 Q 2225
| | | | |

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 925; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKADBDQAGAVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 60
| | | | |
DB 2045 HPEITVKYKADBDQAGAVGYIELDNGSKLIESRPERPFPMSTFKVLLCGAVLSRID 2104
| | | | |
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
| | | | |

Db 2105 AGGOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 2164
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 Q 181
Db 2225 Q 2225

RESULT 14

US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 1999-03-08
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 925; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQAGAVGYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGAVGYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGGOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 120
Db 2105 AGGOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 2164
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 Q 181
Db 2225 Q 2225

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 925; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQAGAVGYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKDAEDQAGAVGYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGGOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 120
Db 2105 AGGOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 2164
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGSELLTLASRQ 180
Db 2165 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVPVAMATTLRKLLTGSELLTLASRQ 2224
QY 181 Q 181
Db 2225 Q 2225

Search completed: June 10, 2005, 11:09:04
Job time : 61.6383 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 57.6231 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPEITVKKVADMDQAGARVG.....RDTMPVAMATTIRKLNGE 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	263	15	US-10-668-778-2
2	885	100.0	286	10	US-09-919-901-7
3	885	100.0	286	10	US-09-919-901-14
4	885	100.0	286	10	US-09-919-901-21
5	885	100.0	286	11	US-09-837-306-354
6	885	100.0	286	14	US-10-191-966-7
7	885	100.0	286	14	US-10-191-966-14
8	885	100.0	286	14	US-10-191-966-21
9	885	100.0	286	15	US-10-045-674-523
10	885	100.0	286	16	US-10-416-708A-73
11	885	100.0	2307	10	US-09-919-901-2

12	885	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	885	100.0	2307	10	US-09-919-901-16	Sequence 16, Appli
14	885	100.0	2307	14	US-10-191-966-2	Sequence 2, Appli
15	885	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	885	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	884	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	884	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
19	884	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	884	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	880	99.4	265	9	US-09-772-114-6	Sequence 6, Appli
22	880	99.4	265	14	US-10-280-482-2	Sequence 2, Appli
23	880	99.4	265	17	US-10-656-029-2	Sequence 2, Appli
24	880	99.4	285	9	US-09-772-114-7	Sequence 7, Appli
25	880	99.4	286	14	US-10-016-668-5	Sequence 5, Appli
26	880	99.4	286	14	US-10-280-482-4	Sequence 4, Appli
27	880	99.4	286	17	US-10-656-029-4	Sequence 4, Appli
28	880	99.4	286	17	US-10-877-952-26	Sequence 26, Appli
29	880	99.4	286	17	US-10-877-952-71	Sequence 71, Appli
30	877	99.1	264	17	US-10-877-952-18	Sequence 18, Appli
31	877	99.1	362	15	US-10-469-199-2	Sequence 2, Appli
32	877	99.1	584	17	US-10-890-675-2	Sequence 2, Appli
33	873	98.6	265	9	US-09-772-114-8	Sequence 8, Appli
34	873	98.6	265	14	US-10-280-482-6	Sequence 6, Appli
35	873	98.6	265	16	US-10-622-088-114	Sequence 114, App
36	873	98.6	265	17	US-10-656-029-6	Sequence 6, Appli
37	873	98.6	265	17	US-10-877-952-154	Sequence 154, App
38	872	98.5	264	9	US-09-772-114-9	Sequence 9, Appli
39	872	98.5	264	14	US-10-280-482-8	Sequence 8, Appli
40	872	98.5	264	17	US-10-656-029-8	Sequence 8, Appli
41	870	98.3	498	17	US-10-491-653-146	Sequence 146, App
42	865.5	97.8	262	14	US-10-177-725-3	Sequence 3, Appli
43	865.5	97.8	262	15	US-10-393-449-3	Sequence 2, Appli
44	846	95.6	284	15	US-10-062-188-2	Sequence 2, Appli
45	463	52.3	94	9	US-09-923-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US20040038317A1
GENERAL INFORMATION:
APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Hong
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%; Score 885; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0;

Qy 1 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 1 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Qy 61 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 61 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Qy 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 172
Db 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 172

RESULT 2

US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 885; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
Qy 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 172
Db 144 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 195

RESULT 3

US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 885; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
Qy 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 172
Db 144 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 195

RESULT 4

US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 885; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVKDADQAGVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQEQGRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
Qy 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 172
Db 144 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDITTMVAAATTLRKLLTGE 195

RESULT 5

US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DVAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCESS5
US-09-837-306-354

Query Match 100.0%; Score 885; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 HPEITVKYKDAEDQAGAVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
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QY 121 KELTSFALNMGDHTRLDRWPELNEAIPNDRDRTTTPVAMATTIRKLLTGE 172
DB 144 KELTSFALNMGDHTRLDRWPELNEAIPNDRDRTTTPVAMATTIRKLLTGE 195

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7
Query Match 100.0%; Score 885; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKDAEDQAGAVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKYKDAEDQAGAVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
DB 84 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 143
QY 121 KELTSFALNMGDHTRLDRWPELNEAIPNDRDRTTTPVAMATTIRKLLTGE 172
DB 144 KELTSFALNMGDHTRLDRWPELNEAIPNDRDRTTTPVAMATTIRKLLTGE 195

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14
Query Match 100.0%; Score 885; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKDAEDQAGAVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPEITVKYKDAEDQAGAVGYIELDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
DB 84 AGQEQIGRIHYSQNDLYEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 143
QY 121 KELTSFALNMGDHTRLDRWPELNEAIPNDRDRTTTPVAMATTIRKLLTGE 172
DB 144 KELTSFALNMGDHTRLDRWPELNEAIPNDRDRTTTPVAMATTIRKLLTGE 195

RESULT 8
US-10-191-966-21
; Sequence 21, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 09/263,933

;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 885; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTIGGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTIGGP 143
QY 121 KETLFLNMGDHVTLRDRWEPELNEAIPNDRDITTMVAAATTLRKLTGE 172
DB 144 KETLFLNMGDHVTLRDRWEPELNEAIPNDRDITTMVAAATTLRKLTGE 195

RESULT 9
US-10-045-674-523
; Sequence 523, Application US/10045674
; Publication No. US200302333A1

;; GENERAL INFORMATION:
;; APPLICANT: LADNER, ROBERT C.
;; APPLICANT: COHEN, EDWARD H.
;; APPLICANT: NASTRI, HORACIO G.
;; APPLICANT: ROONEY, KRISTIN L.
;; APPLICANT: HOFT, RENE
;; APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
;; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
;; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
;; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
;; TITLE OF INVENTION: LIBRARIES
;; FILE REFERENCE: DYAX/002 CIP2
;; CURRENT APPLICATION NUMBER: US/10/045,674
;; CURRENT FILING DATE: 2001-10-25
;; PRIOR APPLICATION NUMBER: 60/198,069
;; PRIOR FILING DATE: 2000-04-17
;; PRIOR APPLICATION NUMBER: 09/837,306
;; PRIOR FILING DATE: 2001-04-17
;; NUMBER OF SEQ ID NOS: 635
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 523
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Vector pCCESS
;; OTHER INFORMATION: protein sequence
US-10-045-674-523

Query Match 100.0%; Score 885; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTIGGP 120

DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTIGGP 143
QY 121 KETLFLNMGDHVTLRDRWEPELNEAIPNDRDITTMVAAATTLRKLTGE 172
DB 144 KETLFLNMGDHVTLRDRWEPELNEAIPNDRDITTMVAAATTLRKLTGE 195

RESULT 10
US-10-416-708A-73
; Sequence 73, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; TITLE OF INVENTION: SPECIFICITIES
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 73
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 885; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.4e-87;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDLSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTIGGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAAILTTIGGP 143
QY 121 KETLFLNMGDHVTLRDRWEPELNEAIPNDRDITTMVAAATTLRKLTGE 172
DB 144 KETLFLNMGDHVTLRDRWEPELNEAIPNDRDITTMVAAATTLRKLTGE 195

RESULT 11
US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1

;; GENERAL INFORMATION:
;; APPLICANT: Potte, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patrick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; CURRENT FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 2307
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-2

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Query Match      100.0%; Score 885; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
        |||
DB      2045 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

QY      61 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
        |||
DB      2105 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

QY      121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 172
        |||
DB      2165 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 2216

RESULT 12
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9

Query Match      100.0%; Score 885; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
        |||
DB      2045 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

QY      61 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
        |||
DB      2105 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

QY      121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 172
        |||
DB      2165 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 2216

RESULT 13
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
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; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16

Query Match      100.0%; Score 885; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
        |||
DB      2045 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

QY      61 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
        |||
DB      2105 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

QY      121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 172
        |||
DB      2165 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 2216

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-2

Query Match      100.0%; Score 885; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.6e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 60
        |||
DB      2045 HPEITLVKVDADQDQAGVGYIELDLSGKILSFPRPFRPMMSTFKVLLCGAVLSRID 2104

QY      61 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 120
        |||
DB      2105 AGOEOLGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTANLLTTIGGP 2164

QY      121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 172
        |||
DB      2165 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDITMPVAMATTAKLTGE 172
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Db 2165 KELTSALHNMGDHVTRLDRWEPBELNEALPNDERDITTMPVAMATTLRKLLTGE 2216

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 885; DB 14; Length 2307;

Best Local Similarity 100.0%; Pred. No. 2.6e-86;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPEITLVKVKDADBDQAGRVGYIELDLNSGKILIESFRPERPRPMSTFKVLLCGAVLSRID 60
|||
DB 2045 HPEITLVKVKDADBDQAGRVGYIELDLNSGKILIESFRPERPRPMSTFKVLLCGAVLSRID 2104
|||
OY 61 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTRELSAATITMSDNTAANLLTTIGAP 120
|||
DB 2105 AGOEOLGRIRIHSQNDLVEYSPVTEKHLTDGWTRELSAATITMSDNTAANLLTTIGAP 2164
|||
OY 121 KELTSALHNMGDHVTRLDRWEPBELNEALPNDERDITTMPVAMATTLRKLLTGE 172
|||
DB 2165 KELTSALHNMGDHVTRLDRWEPBELNEALPNDERDITTMPVAMATTLRKLLTGE 2216
|||

Search completed: June 10, 2005, 11:09:05
Job time : 58.6231 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 49.9177 Seconds
(without alignments)
1144.220 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149
Perfect score: 770
Sequence: 1 HPRTLVKKADBDQ/GARVG.....MGDHTRLDRKPELNEAIP 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1710399 seqs, 383334425 residues
Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17:	/cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19:	/cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	770	100.0	263	15	US-10-668-778-2
2	770	100.0	286	10	US-09-919-901-7
3	770	100.0	286	10	US-09-919-901-14
4	770	100.0	286	10	US-09-919-901-21
5	770	100.0	286	11	US-09-837-306-354
6	770	100.0	286	14	US-10-191-966-7
7	770	100.0	286	14	US-10-191-966-14
8	770	100.0	286	15	US-10-191-966-21
9	770	100.0	286	15	US-10-045-674-523
10	770	100.0	286	16	US-10-416-708A-73
11	770	100.0	2307	10	US-09-919-901-2

12	770	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	770	100.0	2307	10	US-09-919-901-16	Sequence 16, Appli
14	770	100.0	2307	14	US-10-191-966-2	Sequence 2, Appli
15	770	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	770	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	769	99.9	265	9	US-09-772-114-6	Sequence 6, Appli
18	769	99.9	265	14	US-10-280-482-2	Sequence 2, Appli
19	769	99.9	265	17	US-10-656-029-2	Sequence 2, Appli
20	769	99.9	285	9	US-09-772-114-7	Sequence 7, Appli
21	769	99.9	286	14	US-10-016-668-5	Sequence 5, Appli
22	769	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
23	769	99.9	286	14	US-10-280-482-4	Sequence 4, Appli
24	769	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
25	769	99.9	286	17	US-10-656-029-4	Sequence 4, Appli
26	769	99.9	286	17	US-10-877-952-26	Sequence 26, Appli
27	769	99.9	286	17	US-10-877-952-71	Sequence 71, Appli
28	769	99.9	1293	14	US-10-251-385-292	Sequence 292, App
29	769	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
30	762	99.0	264	17	US-10-877-952-18	Sequence 18, Appli
31	762	99.0	362	15	US-10-469-199-2	Sequence 2, Appli
32	762	99.0	584	17	US-10-890-675-2	Sequence 2, Appli
33	758	98.4	265	9	US-09-772-114-8	Sequence 8, Appli
34	758	98.4	265	14	US-10-280-482-6	Sequence 6, Appli
35	758	98.4	265	16	US-10-622-088-114	Sequence 114, App
36	758	98.4	265	17	US-10-656-029-6	Sequence 6, Appli
37	758	98.4	265	17	US-10-877-952-154	Sequence 154, App
38	757	98.3	264	9	US-09-772-114-9	Sequence 9, Appli
39	757	98.3	264	14	US-10-280-482-8	Sequence 8, Appli
40	757	98.3	264	17	US-10-656-029-8	Sequence 8, Appli
41	755	98.1	498	17	US-10-491-653-146	Sequence 146, App
42	750.5	97.5	262	14	US-10-177-725-3	Sequence 3, Appli
43	750.5	97.5	262	15	US-10-393-449-3	Sequence 3, Appli
44	750.5	97.5	284	15	US-10-062-188-2	Sequence 2, Appli
45	393	51.0	94	9	US-09-925-298-760	Sequence 760, App

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US2004003817A1
GENERAL INFORMATION:
APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Hong
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668, 778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526, 106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%; Score 770; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 2,7e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
| | | | |
DB 1 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
| | | | |
DB 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
| | | | |
DB 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149

RESULT 2
US-09-919-901-7

Sequence 7, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potes, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 770; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
| | | | |
DB 24 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
| | | | |
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
| | | | |
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIP 172

RESULT 3
US-09-919-901-14

Sequence 14, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potes, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 770; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
| | | | |
DB 24 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
| | | | |
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
| | | | |
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIP 172

RESULT 4

US-09-919-901-21
Sequence 21, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potes, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
CURRENT APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 770; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
| | | | |
DB 24 HPEITLVKQDAEDDQAGVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
| | | | |
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIP 149
| | | | |
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIP 172

RESULT 5

US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOER, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DVMX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCES5
US-09-837-306-354

Query Match 100.0%; Score 770; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYLEIDLSNGKILSFREPERPPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYLEIDLSNGKILSFREPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGCP 120
DB 84 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTYRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHVTYRLDRWEPELNEAIP 172

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 770; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKDAEDQAGRVGYLEIDLSNGKILSFREPERPPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYLEIDLSNGKILSFREPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGCP 120
DB 84 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTYRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHVTYRLDRWEPELNEAIP 172

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 770; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYLEIDLSNGKILSFREPERPPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYLEIDLSNGKILSFREPERPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGCP 120
DB 84 AGGOLGRRHHYSONDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTYRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHVTYRLDRWEPELNEAIP 172

RESULT 8
US-10-191-966-21
; Sequence 21, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 770; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGVGYIELDLSGKILSFREPRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGVGYIELDLSGKILSFREPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFLNMGDHYTRLDRWEPELNEAIP 172

RESULT 9
US-10-045-674-523
Sequence 523, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DMAX/002.CIP2
CURRENT APPLICATION NUMBER: US/10/045.674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match 100.0%; Score 770; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGVGYIELDLSGKILSFREPRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGVGYIELDLSGKILSFREPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120

DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFLNMGDHYTRLDRWEPELNEAIP 172

RESULT 10
US-10-416-708A-73
Sequence 73, Application US/10416708A
Publication No. US20040161753A1
GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Katja
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416.708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 73
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 770; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGVGYIELDLSGKILSFREPRPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGVGYIELDLSGKILSFREPRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFLNMGDHYTRLDRWEPELNEAIP 172

RESULT 11
US-09-919-901-2
Sequence 2, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Jackson, Karen E.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919.901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-2

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Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRWEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRWEPELNEAIP 2193

RESULT 12
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9

Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRWEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRWEPELNEAIP 2193

RESULT 13
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16

Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRWEPELNEAIP 149
      |||
Db      2165 KELTAFILNMGDHVTRLDRWEPELNEAIP 2193

RESULT 14
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-2

Query Match      100.0%; Score 770; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRWEPELNEAIP 149
      |||
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; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1998-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16

Query Match      100.0%; Score 770; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
      |||
Db      2045 HPELVKVKDADQAGRVGYIELDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 2104

Qy      61 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 120
      |||
Db      2105 AGQEQGRRIHYSQNDLYEVSPTVEKHLTDGMYVELCSAATMSDNTAANLLTTIGSP 2164

Qy      121 KELTAFILNMGDHVTRLDRWEPELNEAIP 149
      |||
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Db 2165 KeltaFLNMGDHYTRLDRWEPDLNEAIP 2193

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patlick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 770; DB 14; Length 2307;

Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDDQGARVGYIELDINSKILIESFRPERPPMSTFKYLICGAVLSRID 60
|||
DB 2045 HPEITLVKTKDAEDDQGARVGYIELDINSKILIESFRPERPPMSTFKYLICGAVLSRID 2104
|||
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTRELCSAITMSDNTAANLLTTIGSP 120
|||
DB 2105 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTRELCSAITMSDNTAANLLTTIGSP 2164
|||
QY 121 KeltaFLNMGDHYTRLDRWEPDLNEAIP 149
|||
DB 2165 KeltaFLNMGDHYTRLDRWEPDLNEAIP 2193
|||

Search completed: June 10, 2005, 11:09:04
Job time : 49.9177 secs

Fri Jun 10 14:22:57 2005

GenCore version 2.00

Pugen Ltd.

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Search time 88.1097 Seconds
(without alignments)
1144.220 Million cell updates/sec

OM protein - protein search, us10

June 10, 2005

Run on: ADJUGARV.....TMDERNROIAIGSLIKHW 263

US:0, Gapext 0.5

Title: Perfect score: 99 seqs, 389334425 residues

Sequence: 1710399

Scoring: Length: 0
eq length: 2000000000Testing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:*

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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1348	100.0	263	15	US-10-668-778-2	Sequence 2, Appli
2	1348	100.0	286	10	US-09-919-901-7	Sequence 7, Appli
3	1348	100.0	286	10	US-09-919-901-14	Sequence 14, Appli
4	1348	100.0	286	10	US-09-919-901-21	Sequence 21, Appli
5	1348	100.0	286	11	US-09-837-306-154	Sequence 34, App
6	1348	100.0	286	14	US-10-191-966-7	Sequence 7, Appli
7	1348	100.0	286	14	US-10-191-966-14	Sequence 14, Appli
8	1348	100.0	286	14	US-10-191-966-21	Sequence 21, Appli
9	1348	100.0	286	15	US-10-045-674-523	Sequence 523, App
10	1348	100.0	286	16	US-10-416-708A-73	Sequence 73, Appli
11	1348	100.0	2307	10	US-09-919-901-2	Sequence 2, Appli

12	1348	100.0	2307	10	US-09-919-901-9	Sequence 9, Appli
13	1348	100.0	2307	10	US-09-919-901-16	Sequence 16, Appli
14	1348	100.0	2307	14	US-10-191-966-2	Sequence 2, Appli
15	1348	100.0	2307	14	US-10-191-966-9	Sequence 9, Appli
16	1348	100.0	2307	14	US-10-191-966-16	Sequence 16, Appli
17	1347	99.9	286	14	US-10-231-013-9	Sequence 9, Appli
18	1347	99.9	286	16	US-10-842-534-9	Sequence 9, Appli
19	1347	99.9	1293	14	US-10-251-385-292	Sequence 292, App
20	1347	99.9	1967	16	US-10-477-044-1	Sequence 1, Appli
21	1343	99.6	265	9	US-09-772-114-6	Sequence 6, Appli
22	1343	99.6	265	14	US-10-280-482-2	Sequence 2, Appli
23	1343	99.6	265	17	US-10-656-029-2	Sequence 2, Appli
24	1343	99.6	285	9	US-09-772-114-7	Sequence 7, Appli
25	1343	99.6	286	14	US-10-016-668-5	Sequence 5, Appli
26	1343	99.6	286	14	US-10-280-482-4	Sequence 4, Appli
27	1343	99.6	286	17	US-10-656-029-4	Sequence 4, Appli
28	1343	99.6	286	17	US-10-877-952-26	Sequence 26, Appli
29	1343	99.6	286	17	US-10-877-952-71	Sequence 71, Appli
30	1340	99.4	264	17	US-10-877-952-18	Sequence 18, Appli
31	1340	99.4	362	15	US-10-469-199-2	Sequence 2, Appli
32	1340	99.4	584	17	US-10-890-675-2	Sequence 2, Appli
33	1336	99.1	265	9	US-09-772-114-8	Sequence 8, Appli
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35	1336	99.1	265	16	US-10-622-088-114	Sequence 114, App
36	1336	99.1	265	17	US-10-656-029-6	Sequence 6, Appli
37	1336	99.1	265	17	US-10-877-952-154	Sequence 154, App
38	1335	99.0	264	9	US-09-772-114-9	Sequence 9, Appli
39	1335	99.0	264	14	US-10-280-482-8	Sequence 8, Appli
40	1335	99.0	264	17	US-10-656-029-8	Sequence 8, Appli
41	1328.5	98.6	262	14	US-10-177-725-3	Sequence 3, Appli
42	1328.5	98.6	262	15	US-10-393-449-3	Sequence 146, App
43	1320	97.9	498	17	US-10-491-653-146	Sequence 2, Appli
44	1299	96.4	284	15	US-10-062-188-2	Sequence 2, Appli
45	584	43.3	118	15	US-10-062-188-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US2004003817A1
GENERAL INFORMATION:
APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Hong
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668, 778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526, 106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURES:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 100.0%; Score 1348; DB 15; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HPELVVVKQABDQAGRVGIEIDLSNGKILSFREPERPMSTFKVLLCGAVLSRID 60
Qy 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
Db 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
Qy 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTMPVMAATTLRKLLTGEILLTASRQ 180
Db 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTMPVMAATTLRKLLTGEILLTASRQ 180
Qy 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAALGPDGKPSRIIVITYTG 240
Db 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAALGPDGKPSRIIVITYTG 240
Qy 241 SOATMDERNRQIAEIGASLIKHW 263
Db 241 SOATMDERNRQIAEIGASLIKHW 263

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RESULT 2

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US-09-919-901-7
Sequence 7, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-919-901-7

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Match 100.0%; Score 1348; DB 10; Length 286;
Qy Similarity 100.0%; Pred. No. 2,4e-125;
Db Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTMPVMAATTLRKLLTGEILLTASRQ 180
Qy 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAALGPDGKPSRIIVITYTG 240
Db 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAALGPDGKPSRIIVITYTG 240
Qy 241 SOATMDERNRQIAEIGASLIKHW 263
Db 241 SOATMDERNRQIAEIGASLIKHW 263

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RESULT 3
US-09-919-901-14
Sequence 14, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-14

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Query Match 100.0%; Score 1348; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-125;
Matches 263; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPELVVVKQABDQAGRVGIEIDLSNGKILSFREPERPMSTFKVLLCGAVLSRID 60
Db 24 HPELVVVKQABDQAGRVGIEIDLSNGKILSFREPERPMSTFKVLLCGAVLSRID 83
Qy 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 120
Db 84 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGCP 143
Qy 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTMPVMAATTLRKLLTGEILLTASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDTMPVMAATTLRKLLTGEILLTASRQ 203
Qy 181 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAALGPDGKPSRIIVITYTG 240
Db 204 QLIIMMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAALGPDGKPSRIIVITYTG 263
Qy 241 SOATMDERNRQIAEIGASLIKHW 263
Db 264 SOATMDERNRQIAEIGASLIKHW 286

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RESULT 4
US-09-919-901-21
Sequence 21, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286

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Fri Jun 10 14:22:57 2005

us-10-668-778-2.rapb

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 1348; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 HPELVKVDADQAGVGYIELDNGSKILESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLLDGMVTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLLDGMVTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 203
QY 181 OLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROJAEIGASLIIKHW 263
DB 264 SOATMDERNROJAEIGASLIIKHW 286

RESULT 5

US-09-837-306-354
Sequence 354, Application US/09837306
Publication No. US20040029113A1
GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOREY, KRISTIN L.
APPLICANT: HOER, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/09/837.306
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 354
LENGTH: 286
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: PC855
US-09-837-306-354

Query Match 100.0%; Score 1348; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 HPELVKVDADQAGVGYIELDNGSKILESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLLDGMVTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLLDGMVTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 180

DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 203
QY 181 OLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROJAEIGASLIIKHW 263
DB 264 SOATMDERNROJAEIGASLIIKHW 286

RESULT 6

US-10-191-966-7
Sequence 7, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:

APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191.966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263.933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1348; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 HPELVKVDADQAGVGYIELDNGSKILESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIHYSQNDLVEYSPVTEKHLLDGMVTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOELGRRIHYSQNDLVEYSPVTEKHLLDGMVTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTYRKLLTGELTLASRQ 203
QY 181 OLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROJAEIGASLIIKHW 263
DB 264 SOATMDERNROJAEIGASLIIKHW 286

RESULT 7

US-10-191-966-14
Sequence 14, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:

APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 1348; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAGIASLIRHW 263
DB 264 SOATMDERNROIAGIASLIRHW 286

RESULT 8
US-10-191-966-21
Sequence 21, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-21

Query Match 100.0%; Score 1348; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNROIAGIASLIRHW 263
DB 264 SOATMDERNROIAGIASLIRHW 286

RESULT 9
US-10-045-674-523
Sequence 523, Application US/10045674
Publication No. US2003023333A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROONEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
US-10-045-674-523

Query Match 100.0%; Score 1348; DB 15; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDINSKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTMPVAMATTIRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDMMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263

QY 241 SOATMDERNROIAEIGASLIKHM 263
DB 264 SOATMDERNROIAEIGASLIKHM 286

RESULT 10

US-10-416-708A-73
; Sequence 73, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Frommnecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-73

Query Match 100.0%; Score 1348; DB 16; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,4e-125;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIELDLSNGKILIESRPERPMPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGAVGYIELDLSNGKILIESRPERPMPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVEILCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVEILCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGELTLASRQ 203
QY 161 QUIDMWEADKVAQPLRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 240
DB 204 QUIDMWEADKVAQPLRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 263
QY 241 SOATMDERNROIAEIGASLIKHM 263
DB 264 SOATMDERNROIAEIGASLIKHM 286

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 1348; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIELDLSNGKILIESRPERPMPMSTFKVLLCGAVLSRID 60
DB 2045 HPEITLVKVKADBDQAGAVGYIELDLSNGKILIESRPERPMPMSTFKVLLCGAVLSRID 2104
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVEILCSAATMSDNTAANLLTTIGSP 120
DB 2105 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVEILCSAATMSDNTAANLLTTIGSP 2164
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGELTLASRQ 180
DB 2165 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGELTLASRQ 2224
QY 181 QUIDMWEADKVAQPLRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 240
DB 2225 QUIDMWEADKVAQPLRSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITTG 2284
QY 241 SOATMDERNROIAEIGASLIKHM 263
DB 2285 SOATMDERNROIAEIGASLIKHM 2307

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 1348; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIELDLSNGKILIESRPERPMPMSTFKVLLCGAVLSRID 60
DB 2045 HPEITLVKVKADBDQAGAVGYIELDLSNGKILIESRPERPMPMSTFKVLLCGAVLSRID 2104
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVEILCSAATMSDNTAANLLTTIGSP 120
DB 2105 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVEILCSAATMSDNTAANLLTTIGSP 2164
QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGELTLASRQ 180

Db 2165 KETFAFLHMGDHYRLDRWEPELNEAIPNDERDTTMAPVAAATTKLLTGELLTLASRQ 2224
QY 181 QUIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
Db 2225 QUIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 2284
QY 241 SOATWDERNRQIAEIGASLIGKM 263
Db 2285 SOATWDERNRQIAEIGASLIGKM 2307

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 1348; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQUGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 2045 HPELVKVKDAEDQUGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQGRRIHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 120
Db 2105 AGQEQGRRIHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 2164
QY 121 KETFAFLHMGDHYRLDRWEPELNEAIPNDERDTTMAPVAAATTKLLTGELLTLASRQ 180
Db 2165 KETFAFLHMGDHYRLDRWEPELNEAIPNDERDTTMAPVAAATTKLLTGELLTLASRQ 2224
QY 181 QUIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
Db 2225 QUIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 2284
QY 241 SOATWDERNRQIAEIGASLIGKM 263
Db 2285 SOATWDERNRQIAEIGASLIGKM 2307

RESULT 14

US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 1348; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQUGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 2045 HPELVKVKDAEDQUGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQGRRIHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 120
Db 2105 AGQEQGRRIHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGGP 2164
QY 121 KETFAFLHMGDHYRLDRWEPELNEAIPNDERDTTMAPVAAATTKLLTGELLTLASRQ 180
Db 2165 KETFAFLHMGDHYRLDRWEPELNEAIPNDERDTTMAPVAAATTKLLTGELLTLASRQ 2224
QY 181 QUIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
Db 2225 QUIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 2284
QY 241 SOATWDERNRQIAEIGASLIGKM 263
Db 2285 SOATWDERNRQIAEIGASLIGKM 2307

RESULT 15

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 1348; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 4,6e-124;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HPELVKVDABEDOLGARVGYIELDLSGKILESFRPERPMMSTFKVLLCGAVLSRID 60
      |||||||
Db      2045 HPELVKVDABEDOLGARVGYIELDLSGKILESFRPERPMMSTFKVLLCGAVLSRID 2104
      |||||||
Qy      61 AGQEOIGRRIRHSQNDLVESPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
      |||||||
Db      2105 AGQEOIGRRIRHSQNDLVESPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 2164
      |||||||
Qy      121 KELTAFLHNMGDHVTRLDRWPELNEAIPNDERDITMPVAMATTLRKLLTGEILTLASRQ 180
      |||||||
Db      2165 KELTAFLHNMGDHVTRLDRWPELNEAIPNDERDITMPVAMATTLRKLLTGEILTLASRQ 2224
      |||||||
Qy      161 QLIDMNEADKVAGPILRSALPAGMFIADKSGAGERSGIIAALGPDGKPSRIIVVITYTG 240
      |||||||
Db      2225 QLIDMNEADKVAGPILRSALPAGMFIADKSGAGERSGIIAALGPDGKPSRIIVVITYTG 2284
      |||||||
Qy      241 SQATMDERNRQIAEIGASLIIKHM 263
      |||||||
Db      2285 SQATMDERNRQIAEIGASLIIKHM 2307
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Search completed: June 10, 2005, 11:09:03
 Job time : 89.1097 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:22:36 ; Search time 57.7711 Seconds
(without alignments)
997.510 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149

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Sequence: 1 HPELVVAVKXAEADQAGARVG.....MGDHTVLRDREPELNEAIP 149

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

2105692

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19908:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	770	100.0	263 4 AAB05544	Aa05544 E. coli m
2	770	100.0	263 4 AAB36592	Aab36592 Escherich
3	770	100.0	263 8 AD067709	Ad067709 Escherich
4	770	100.0	264 2 AAM16634	Aam16634 Beta-lact
5	770	100.0	264 2 AAM18680	Aam18680 Intracell
6	770	100.0	264 2 AAR31575	Aar31575 Ampicilli
7	770	100.0	286 2 AAR97619	Aar97619 Secretory
8	770	100.0	286 2 AAR96423	Aar96423 Cytochrom
9	770	100.0	286 2 AAM16635	Aam16635 Beta-lact
10	770	100.0	286 2 AAM18679	Aam18679 Secretory
11	770	100.0	286 2 AAY08529	Aay08529 Vector pA
12	770	100.0	286 2 AAB10442	Aab10442 Expressio
13	770	100.0	286 3 AAB10438	Aab10438 Expressio
14	770	100.0	286 3 AAB10440	Aab10440 Expressio
15	770	100.0	286 4 AAB50898	Aab50898 Protein e
16	770	100.0	286 4 AAB31173	Aab31173 Amino aci
17	770	100.0	286 5 AAV75551	AAV75551 cel2 inte
18	770	100.0	286 5 AAB55474	Aab55474 Vector pC
19	770	100.0	286 6 ABR43622	ABr43622 Cloning v
20	770	100.0	286 8 ADR70422	Adr70422 Vector pA
21	770	100.0	286 8 ADR70410	Adr70410 Vector pA
22	770	100.0	286 8 ADR70404	Adr70404 Vector pA
23	770	100.0	286 8 ADR70416	Adr70416 Vector pA
24	770	100.0	286 8 ADR70428	Adr70428 Vector pA
25	770	100.0	290 4 AAU23219	AAu23219 Novel hum

ALIGNMENTS

RESULT 1	
ID AAE05544	AAE05544 standard; protein, 263 AA.
XX AC AAE05544;	
XX DT 24-SEP-2001	(first entry)
XX DE E. coli mature TEM-1 beta-lactamase.	
XX DE	
KW Interaction-dependent enzyme association; IdeA system; biosensor;	
KW circularly permuted interaction-activated protein; marker protein;	
KW type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;	
KW therapeutic; drug screening; thiodoxin; ampicillin resistance.	
XX ES Escherichia coli.	
OS	
XX Key	Location/Qualifiers
XX FH Cleavage-site	27. .28
XX FT /note= "Break-point between alpha and omega fragments"	36. .40
XX FT Region	36. .40
XX FT /note= "Inter-sub-domain loop"	38. .39
XX FT Cleavage-site	38. .39
XX FT /note= "Break-point between alpha and omega fragments"	45
XX FT Active-site	74. .75
XX FT /note= "Break-point between alpha and omega fragments"	149. .150
XX FT Cleavage-site	149. .150
XX FT /note= "Break-point between alpha and omega fragments"	172. .173
XX FT Cleavage-site	172. .173
XX FT /note= "Break-point between alpha and omega fragments"	189. .204
XX FT Region	189. .204
XX FT /note= "Inter-sub-domain loop"	190. .191
XX FT Cleavage-site	190. .191
XX FT /note= "Break-point between alpha and omega fragments"	202. .203
XX FT Cleavage-site	202. .203
XX FT /note= "Break-point between alpha and omega fragments"	228. .229
XX FT Cleavage-site	228. .229
XX FT /note= "Break-point between alpha and omega fragments"	
XX PD WO200151629-A2.	
XX PN 19-JUL-2001.	
XX PF 16-JAN-2001; 2001WO-US001651.	
XX PR 13-JAN-2000; 2000US-0175968P.	
XX PR 15-MAR-2000; 2000US-00526106.	

ID ADJ67709 standard; protein; 263 AA.
 XX ADJ67709;
 AC 20-MAY-2004 (first entry)
 DT
 XX
 DE Escherichia coli TEM-1 beta-lactamase.
 XX
 KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX Escherichia coli.
 OS
 XX US2004038317-A1.
 PN
 XX 26-FEB-2004.
 PD
 XX 22-SEP-2003; 2003US-00668778.
 PF
 XX 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135925P.
 PR 15-JAN-2000; 2000US-0175968P.
 PR 15-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIO INC.
 XX
 PI Balint RF, Her J;
 PI WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 DR
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 PS
 XX Disclosure; SEQ ID NO 2; 47bp; English.
 XX
 CC The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and reassemble
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneous incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;
 CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)
 CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 CC
 CC Sequence 263 AA;

Query Match 100.0%; Score 770; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 7.9e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPETLVKVKDAEDGVGVYIETDLSGKILLESFRRPEPPPMSTFVLLCGAVLSRID 60
 DB 1 HPETLVKVKDAEDGVGVYIETDLSGKILLESFRRPEPPPMSTFVLLCGAVLSRID 60
 QY 61 AGQELGRIRIYSQNDLVEYSPVTRKHLTDGMTVRELCSAIIYMGSDNTAANILLTTIGSP 120
 DB 61 AGQELGRIRIYSQNDLVEYSPVTRKHLTDGMTVRELCSAIIYMGSDNTAANILLTTIGSP 120
 QY 121 KEITAFLEHMGDHYTRLDRWEPELNEAIP 149
 DB 121 KEITAFLEHMGDHYTRLDRWEPELNEAIP 149
 RESULT 4
 AAM16634
 ID AAM16634 standard; protein; 264 AA.
 XX
 AC AAM16634;
 XX
 DT 09-AUG-1997 (first entry)
 DE Beta-lactamase (including signal peptide).
 XX
 KM Gene directed enzyme prodnrg therapy; GDEPT;
 KM virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide
 XX
 PN MO9719180-A2.
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96MO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;
 XX
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 PS
 XX Example; Page 28; 38pp; English.
 XX
 CC Escherichia coli beta-lactamase (AAM16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnrg therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodnrg into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill
 XX
 XX Sequence 264 AA;

Query Match 100.0%; Score 770; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 7.9e-80;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 HPELVKVKADBDQAGARVGIETLDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB      2 HPELVKVKADBDQAGARVGIETLDNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
QY      61 AGOGLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGP 120
DB      62 AGOGLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGP 121
QY      121 KELTAFILNMGDHYTRLDRWEPELNEAIP 149
DB      122 KELTAFILNMGDHYTRLDRWEPELNEAIP 150

RESULT 5
AAW18680
ID      AAW18680 standard; protein; 264 AA.
XX
XX      AAW18680;
XX
XX      13-AUG-1997 (first entry)
XX
XX      Intracellularly-expressed beta-lactamase.
XX
XX      Producing therapy; gene directed enzyme producing therapy; GDEPT;
XX      virus directed enzyme producing therapy; VDEPT; lung cancer;
XX      beta-lactamase; PCMV-delIBL.
XX      Escherichia coli.
XX      MO9719183-A2.
XX
XX      29-MAY-1997.
XX
XX      19-NOV-1996; 96WO-GB002846.
XX
XX      20-NOV-1995; 95GB-00023703.
XX
XX      (GLAX ) GLAXO GROUP LTD.
XX
XX      Dev I, Moore JT, Sethna PB;
XX
XX      WPI; 1997-298118/27.
XX
XX      N-PSDB; AAT70311.
XX
XX      DNA construct for gene-directed enzyme producing therapy of lung cancer -
XX      comprises lung- or neuroendocrine-specific promoter controlling
XX      expression of producing-converting enzyme.
XX
XX      Example 8111; Page 32-34; 53pp; English.
XX
XX      The intracellular form (AAW18680) of TEM beta-lactamase is expressed by
XX      PCMV-delIBL (AAT70311) in which a PCR-amplified beta-lactamase coding
XX      sequence, minus the signal sequence, is placed under control of the
XX      intermediate/early promoter of cytomegalovirus. Intracellular beta-
XX      lactamase constructs, placed under control of promoter/enhancer elements
XX      of lung-associated protein or neuroendocrine marker protein genes, can be
XX      used in novel chimeric molecules for use in producing therapy of lung
XX      cancer
XX
XX      Sequence 264 AA;
XX
Query Match      100.0%; Score 770; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 7.9e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      121 KELTAFILNMGDHYTRLDRWEPELNEAIP 149
DB      122 KELTAFILNMGDHYTRLDRWEPELNEAIP 150

RESULT 6
AAR31575
ID      AAR31575 standard; protein; 286 AA.
XX
XX      AAR31575;
XX
XX      10-MAR-2003 (revised)
XX      04-JUN-1993 (first entry)
XX
XX      Ampicillin resistance protein.
XX
XX      CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;
XX      xenobiotics; circular; chimeric cytochrome P450IA1.
XX
XX      Homo sapiens.
XX
XX      US5180666-A.
XX
XX      19-JAN-1993.
XX
XX      27-JUN-1991; 91US-00721775.
XX
XX      27-JUN-1991; 91US-00721775.
XX
XX      (UYWA-) UNIV WAYNE STATE.
XX
XX      States JC, Hines RM, Novak RF;
XX
XX      WPI; 1993-052845/06.
XX
XX      N-PSDB; AAQ36498.
XX
XX      In vitro method for testing mutagenicity of a chemical - by metabolizing
XX      chemical cell line consisting of transformed fibroblasts having
XX      detectable cytochrome P450 mixed function oxidase activity and detecting
XX      gene damage.
XX
XX      Disclosure; Col 21-24; 24pp; English.
XX
XX      The expression constructs PRNH127 and PRNH155 contain identical sequences
XX      but were constructed using different strategies (see AAQ36498). The
XX      constructs comprise exons 2-7 of human CYP1A1 gene under the control of
XX      the inducible mouse metallothionein (MT-1) promoter. The constructs also
XX      contain an open reading frame in the opposite orientation to the
XX      cytochrome P450 exons. This ORF encodes ampicillin resistance. The
XX      constructs are suitable for transformation of human fibroblasts derived
XX      from the xeroderma pigmentosum group A. Cultures of the transformed
XX      fibroblasts can be used to test substances for mutagenicity. The presence
XX      of the inducible cytochrome P450 gene allows metabolism of the substance
XX      to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
XX      field.)
XX
XX      Sequence 286 AA;
XX
Query Match      100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

DB 144 KELTAFILNMGDHVTRLDRWPELNEAIP 172

RESULT 7
AAR97619
ID AAR97619 standard; protein; 286 AA.
XX AAR97619;
AC
XX
XX 20-AUG-1996 (first entry)
DT
XX
XX
DE Secretory beta-lactamase.
XX
XX Gene therapy; gene directed enzyme prodnug therapy; GDEPT;
KM virus directed enzyme prodnug therapy; VDEPT; prodnug activation;
KM cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
KM beta-lactamase; cephalosporin.
XX
XX Synthetic.
OS
XX MO616179-A1.
PN
XX 30-MAY-1996.
PD
XX 20-NOV-1995; 95WO-GB002716.
PF
XX 18-NOV-1994; 94GB-00023367.
PR
XX (WELL) WELLCOME FOUND LTD.
PA
XX
XX Dev IK, Moore JT, Ohmsted C;
PI
XX WPI; 1996-268615/27.
DR N-PSDB; AAT29220.
XX
XX Molecular chimaera for use in enzyme gene therapy - is activated in a
PT target cell to express a secretible enzyme which cleaves a prodnug
PT outside the cell into a cytotoxic or cytostatic agent.
PT
XX
XX Example 3; Page 57-58; 73pp; English.
PS
XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct
CC PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under
CC the control of the intermediate/early cytomegalovirus promoter. Beta-
CC lactamase delivery to mammalian cells confers sensitivity to
CC cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations
CC resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival
CC of mice bearing human large cell lung H460 intrathoracic (i.e.) tumours
CC was increased upon i.t. injection of the secretory beta-lactamase DNA
CC construct
CC
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKXVDADQAGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEBOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGQEBOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIP 149
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIP 172

RESULT 8
AAR96423
ID AAR96423 standard; protein; 286 AA.

XX AAR96423;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 25-NOV-1996 (first entry)
DT
XX
XX Cytochrome P450 (CYP1A1 construct).
DE
XX
XX cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KM metabolism.
XX
XX Homo sapiens.
OS
XX US5525482-A.
PN
XX 11-JUN-1996.
PD
XX 15-NOV-1994; 94US-00339658.
PF
XX 27-JUN-1991; 91US-00721775.
PR 09-DEC-1992; 92US-00990295.
XX
XX (UYWA-) UNIV WAYNE STATE.
PA
XX
XX Hines RN, Novak RF, States JC;
PI
XX WPI; 1996-286397/29.
DR N-PSDB; AAT30354.
XX
XX Testing chemicals for cytotoxicity to human by detecting gene damage -
PT using recombinant fibroblasts transformed with cytochrome P450 gene under
PT control of inducible promoter.
PT
XX
XX Disclosure; Col 17-24; 26pp; English.
PS
XX
XX The present sequence is encoded by a chimeric mouse metallothionein-
CC cytochrome P450Ia1 (CYP1A1) expression construct. Two clones, pRNM127 and
CC pRNM15, were isolated by different methods and which both had the same
CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
CC of humans to a chemical. The method comprises exposing human fibroblast
CC cells normally not including any cytochrome P450 activity to potentially
CC toxic chemicals. The cells having been transformed to express cytochrome
CC P450, under the control of a controllable promoter through the CYP1A1
CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
CC intracellularly into a cytochrome metabolite by oxidation within the
CC fibroblasts through the intracellular cytochrome P450 mixed function
CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8.8e-80;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKXVDADQAGARVGYIELDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGQEBOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGQEBOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIP 149
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIP 172

RESULT 9
AAW16635
ID AAW16635 standard; protein; 286 AA.
XX

```

AC AAW16635;
XX
XX 09-AUG-1997 (first entry)
XX
XX Beta-lactamase (no signal peptide).
XX
XX Gene directed enzyme prodnrg therapy; GDEPT;
XX virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
XX HIV; inflammation.
XX
XX Escherichia coli.
XX
XX WO9719180-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002845.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Ohmstede C;
XX
XX WPI; 1997-298117/27.
XX
XX N-PSDB; AAT66737.
XX
XX Molecular chimera for gene or virus directed enzyme prodnrg therapy -
XX useful for treatment of cancer, viral infection or inflammation.
XX
XX Example; Page 26; 38pp; English.
XX
XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
XX is the expression product of a molecular chimera, designated PCMV-delBL
XX (AAT66738), in which the beta-lactamase gene is under control of the CMV
XX intermediate/early promoter. Vectors consisting of a transcriptional
XX regulatory DNA sequence linked to a beta-lactamase gene can be used for
XX enzyme prodnrg therapy. Intracellular expression of the beta-lactamase in
XX a targeted cell allows conversion of a prodnrg into an agent toxic to
XX the cell for treatment of cancer, viral (e.g. HIV) infection or
XX inflammation.
XX
XX Sequence 286 AA;
XX
XX SQ
XX
XX Query Match 100.0%; Score 770; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-80;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HPEITLVKVKADBDQAGARVGYIELDLSNGKILBSFRPERPPMSTFKVLLCGAVLSRID 60
XX |||||||
XX DB 24 HPEITLVKVKADBDQAGARVGYIELDLSNGKILBSFRPERPPMSTFKVLLCGAVLSRID 83
XX
XX QY 61 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 120
XX |||||||
XX DB 84 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 143
XX
XX QY 121 KETLTAFLNMGDHYTRLDRWEPLEINAI 149
XX |||||||
XX DB 144 KETLTAFLNMGDHYTRLDRWEPLEINAI 172
XX
XX
XX RESULT 10
XX AAW18679
XX ID AAW18679 standard; protein; 286 AA.
XX
XX AC AAW18679;
XX
XX XX 13-AUG-1997 (first entry)
XX
XX XX Secretory beta-lactamase.
XX
XX DE Secretory beta-lactamase.
XX
XX XX Prodnrg therapy; gene directed enzyme prodnrg therapy; GDEPT;
XX virus directed enzyme prodnrg therapy; VDEPT; lung cancer;
XX

```

```

KM beta-lactamase; PCMV-BL.
XX
XX Escherichia coli.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein 24..286
XX /label= sig_peptide
XX /label= Mat_protein
XX
XX WO9719183-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002846.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Sethna PB;
XX
XX WPI; 1997-298118/27.
XX
XX N-PSDB; AAT70309.
XX
XX DNA construct for gene-directed enzyme prodnrg therapy of lung cancer -
XX comprises lung- or neuroendocrine-specific promoter controlling
XX expression of prodnrg-converting enzyme.
XX
XX Example 81; Page 26-27; 53pp; English.
XX
XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by PCMV-
XX BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
XX placed under control of the intermediate/early promoter of
XX cytomegalovirus. Secretory beta-lactamase constructs, placed under
XX control of promoter/enhancer elements of lung- associated protein or
XX neuroendocrine marker protein genes, can be used in novel chimeric
XX molecules for use in prodnrg therapy of lung cancer
XX
XX Sequence 286 AA;
XX
XX SQ
XX
XX Query Match 100.0%; Score 770; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-80;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HPEITLVKVKADBDQAGARVGYIELDLSNGKILBSFRPERPPMSTFKVLLCGAVLSRID 60
XX |||||||
XX DB 24 HPEITLVKVKADBDQAGARVGYIELDLSNGKILBSFRPERPPMSTFKVLLCGAVLSRID 83
XX
XX QY 61 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 120
XX |||||||
XX DB 84 AGOQOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGCP 143
XX
XX QY 121 KETLTAFLNMGDHYTRLDRWEPLEINAI 149
XX |||||||
XX DB 144 KETLTAFLNMGDHYTRLDRWEPLEINAI 172
XX
XX
XX RESULT 11
XX AAY08529
XX ID AAY08529 standard; protein; 286 AA.
XX
XX AC AAY08529;
XX
XX XX 03-AUG-1999 (first entry)
XX
XX XX Vector pASK75 beta-la protein.
XX
XX DE Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
XX tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
XX insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
XX allergy.
XX

```

OS Synthetic.
XX
XX W09925866-A1.
XX
XX 27-MAY-1999.
XX
XX 11-NOV-1998; 98WO-F1000873.
XX
XX 14-NOV-1997; 97FI-00004235.
XX
XX (KORP/) Korpela M.
XX (KARP/) Karp M.
XX (KURIT/) Kurittu J.
XX
XX Korpela M, Karp M, Kurittu J;
XX
XX WPI; 1999-338015/28.
XX
XX N-PSDB; AAV72418.
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
XX
XX
XX Disclosure; Page 47-48; 67pp; English.
XX
XX This invention describes a novel tetracycline assay that uses recombinant
XX prokaryotic cells comprising a luciferase gene under the transcriptional
XX control of a tetracycline repressor and tetracycline promoter and
XX involves the detection of luminescence emitted from the cells. The assay
XX can be used to distinguish tetracycline form other microbial agents. The
XX invention also describes a novel plasmid comprising either the luxDABG
XX genes, a tetracycline repressor (Tetr) and a tetracycline promoter (Tetr)
XX from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
XX and a tetracycline promoter (Tetr) from Tn10. The tetracycline assay
XX method can be used for the determination of tetracycline in a sample,
XX e.g. to study the dosage and penetration of the medicine. The method can
XX also be used to test cheese production, as cheese making bacteria are not
XX able to work in the presence of tetracycline. The method can also be used
XX to determine the presence or concentration of antibiotics in foodstuffs,
XX e.g. for allergic people. The present assay method does not rely on the
XX growth of microbes as do conventional tests, and so is much more rapid.
XX The present assay is also more sensitive, as even a small amount of
XX luminescence can be detected
XX
XX Sequence 286 AA;
XX
XX Query Match 100.0%; Score 770; DB 2; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-80;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HPEITLVKRDADDOUGARVGYIELDNLNGKILSFRRPRRPPMSTFVVLGAVLSRID 60
XX |||||||
XX 24 HPEITLVKRDADDOUGARVGYIELDNLNGKILSFRRPRRPPMSTFVVLGAVLSRID 83
XX
XX 61 AGOEOLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
XX 84 AGOEOLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
XX
XX 121 KELTSFLHNMGDHVTRLDRWEPELNEAIP 149
XX |||||||
XX 144 KELTSFLHNMGDHVTRLDRWEPELNEAIP 172
XX
XX
XX RESULT 12
XX AAB10442
XX ID AAB10442 standard; protein; 286 AA.
XX
XX AC AAB10442;
XX
XX DT 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX15G2 bla protein.
XX
XX DE Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX
XX OS Synthetic.
XX
XX DE19900635-A1.
XX
XX 13-JUL-2000.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Beltling F, Poustka A, Moldenhauer G;
XX
XX WPI; 2000-499832/45.
XX
XX N-PSDB; AAA71430.
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
XX hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.
XX
XX Claim 16; Fig 3; 22pp; German.
XX
XX This invention describes a novel method for the selection of monoclonal
XX antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
XX cells to produce antibody-producing hybridomas such that the antibodies
XX are presented at the surface of the hybridomas by an antibody-binding
XX protein (i); and (ii) binding the antibody to antigens (Ag). The
XX invention also describes antibody-binding proteins (i) that comprise a
XX combination of the signal peptide of a murine immunoglobulin (Ig) kappa
XX chain or a murine MHC (major histocompatibility complex) Class I K(Ik)
XX molecule; an antibody-binding site of proteins A, G, I or Ig, and the
XX transmembrane domain of PDGFR (platelet-derived growth factor receptor)
XX or CD52. The method is used to select Mab with specificity for particular
XX antigens. Mab can be selected without separate culture of hybridomas, and
XX selection can be made against many antigens in a library, optionally on
XX the basis of strength of affinity for a particular antigen. Complex
XX mixtures of hybridomas can be used for selection, reducing the time and
XX cost involved in Mab selection. This sequence represents the bla protein
XX contained in the expression vector pSEX15G2 which contains the
XX bla protein, Neo-R and protein G described in the method of the invention
XX
XX Sequence 286 AA;
XX
XX Query Match 100.0%; Score 770; DB 3; Length 286;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-80;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HPEITLVKRDADDOUGARVGYIELDNLNGKILSFRRPRRPPMSTFVVLGAVLSRID 60
XX |||||||
XX 24 HPEITLVKRDADDOUGARVGYIELDNLNGKILSFRRPRRPPMSTFVVLGAVLSRID 83
XX
XX 61 AGOEOLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
XX 84 AGOEOLGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
XX
XX 121 KELTSFLHNMGDHVTRLDRWEPELNEAIP 149
XX |||||||
XX 144 KELTSFLHNMGDHVTRLDRWEPELNEAIP 172
XX
XX
XX RESULT 13
XX AAB10438
XX ID AAB10438 standard; protein; 286 AA.
XX
XX AC AAB10438;
XX
XX DT 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX11L4 bla protein.
XX
XX DE Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

XX bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; cell gene,
KW glucanase; integration vector; pIO13306.

OS Unidentified.

PN WO200071729-A2.

PD 30-NOV-2000

PF 26-MAY-2000; 2000WO-US014773.

PR 26-MAY-1999; 99US-0136376P.

PA (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;

DR WPI; 2001-032043/04.

XXIX

PT Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.

PS Disclosure; Page 82-83; 87pp; English

The present sequence is given in a specification relating to a recombinant host cell suitable for simultaneous saccharification and fermentation. The host cell contains at least one heterologous polynucleotide encoding a polysaccharase under the transcriptional control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polynucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharases which is useful for enzymatically degrading oligosaccharides such as laminaribiose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from *Zymomonas mobilis*, the *celZ* gene from *Erythra chrysanthemi*, resistance markers *bla* and *tet*, and *Klebsiella oxytoca* target sequence

SQ Sequence 286 AA;

Query Match	100.0%;	Score 770;	DB 4;	Length 286;
-------------	---------	------------	-------	-------------

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKKAEDQLGARVGIIBLDNSGKILSFRRPEERFPMSTFKVLLCGAVLSRID 600

Db 24 HPETLVKVDADQLGARVGIIBLDINSGKILESFRPEERFPMSTFKVLLCGAVLSRID 83

61 AGOEOLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTAANLLTTIGGP 120

Db 84 AGQEQIGRIHYSQNDLVESPTBKHLTDGMTVRELCSAITSMDNTANLLTTIGP 143

121 KETAPLHNMGDVTRLDREPELNEAIP 149

Db 144 KETAFLEHMGDHTRLDRWEPELNEAIP 172

Search completed: June 10, 2005, 10:49:11
Job time : 58.7711 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 88.1097 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2

Perfect score: 1348
Sequence: 1 HPELVKVKVADQAGARVG.....TMDERNRQIAETGASLIKHW 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	286	2	Q38058 bacteriophage Q38058
2	1348	100.0	286	2	Q00626 Staphylococcus aureus
3	1348	100.0	286	2	Q79CL6 methylobacterium
4	1348	100.0	286	2	Q79DR3 Escherichia coli
5	1343	99.6	286	1	BLAT_ECOLI
6	1343	99.6	286	1	BLAT_SALTI
7	1343	99.6	286	2	Q6A253
8	1343	99.6	286	2	Q6LBN9
9	1343	99.6	286	2	Q6LVC6
10	1343	99.6	286	2	Q6TMM1
11	1343	99.6	286	2	Q6WRX2
12	1343	99.6	286	2	Q6WRX2
13	1343	99.6	286	2	Q6WZD4
14	1343	99.6	286	2	Q7B3X5
15	1343	99.6	286	2	Q7B899
16	1343	99.6	286	2	Q7B899
17	1343	99.6	286	2	Q7B875
18	1343	99.6	286	2	Q7DFY3
19	1343	99.6	286	2	Q7DHD3
20	1343	99.6	286	2	Q799Y1
21	1343	99.6	286	2	Q7BVP8
22	1340	99.4	286	2	Q8KSD2
23	1339	99.3	286	2	Q3J372
24	1339	99.3	286	2	Q8KSD3
25	1339	99.3	286	2	Q932Y6
26	1339	99.3	286	2	Q93A80
27	1339	99.3	286	2	Q6QCR1
28	1339	99.3	286	2	Q6SQJ9
29	1339	99.3	286	2	Q6URK84
30	1339	99.3	286	2	Q6UVM7
31	1339	99.3	286	2	Q6W7J4

32	1339	99.3	286	2	Q7B0V0	O7B0V0 xanthomonas
33	1339	99.3	286	2	Q9RM52	Q9RM52 escherichia
34	1339	99.3	286	2	Q9RM48	Q9RM48 escherichia
35	1338	99.3	286	2	Q8KRH0	Q8KRH0 klebsiella
36	1338	99.3	286	2	Q93A77	Q93A77 escherichia
37	1338	99.3	286	2	Q9R745	Q9R745 escherichia
38	1337	99.2	285	2	Q6KX67	Q6KX67 hordium vul
39	1337	99.2	286	2	Q8YP43	Q8YP43 klebsiella
40	1337	99.2	286	2	Q48406	Q48406 klebsiella
41	1337	99.2	286	2	Q6ZYM6	Q6ZYM6 salmoneila
42	1337	99.2	286	2	Q844X1	Q844X1 klebsiella
43	1337	99.2	286	2	Q8G485	Q8G485 escherichia
44	1337	99.2	286	2	Q96678	Q96678 klebsiella
45	1336	99.1	286	2	P78144	P78144 escherichia

ALIGNMENTS

RESULT 1

ID Q38058 PRELIMINARY; PRT; 286 AA.
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta lactamase.
GN Name=bla;
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95172401; Pubmed=7867948; DOI=10.1016/0378-1119(94)00839-K;
RA Hendrich B., Schmidtberger B.;
RT "A variant of phix174 gene E-based positive selection vectors with
enhanced lytic potential.";
RL Gene 154:51-54 (1995).
DR EMBL; Z35638; CAA84692.1; -.
DR PIR; S47061; S47061.
DR HSSP; Q9R435; 1HT2.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000671; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5BB2F22753375FA9 CRC64;

Query Match

Best Local Similarity 100.0%; Score 1348; DB 2; Length 286;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPELVKVKVADQAGARVGYLELDLNSGKILIESFRPERFPMSTPKVLLCGAVLSRID	60
DB	24	HPELVKVKVADQAGARVGYLELDLNSGKILIESFRPERFPMSTPKVLLCGAVLSRID	83
QY	61	AGQEQGLRRIRHSQNDLVYSPVTEKHLLTDGTTVAELCSAATMNDNPAANLLTTIGCP	120
DB	84	AGQEQGLRRIRHSQNDLVYSPVTEKHLLTDGTTVAELCSAATMNDNPAANLLTTIGCP	143
QY	121	KELTAFILNMGDHYRLRWBPENLEALPNDERDITPMVAMATTIRKLLTGLTLTASRQ	180
DB	144	KELTAFILNMGDHYRLRWBPENLEALPNDERDITPMVAMATTIRKLLTGLTLTASRQ	203
QY	181	QIIDWEADKVAQPLRLSALPAWPIADKSGAGERSGIIAALGPDGKPSRIIVITYTG	240
DB	204	QIIDWEADKVAQPLRLSALPAWPIADKSGAGERSGIIAALGPDGKPSRIIVITYTG	263
QY	241	SOATMDERNRQIAETGASLIKHW 263	
DB	264	SOATMDERNRQIAETGASLIKHW 286	

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RESULT 2
ID 000626 PRELIMINARY: PRT: 286 AA.
AC 000626: 008022; 008102; 009393; 009396; 009397; 009398; 009399;
AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
AC 009408; 009481; 009482; 009483; 009490; 057339;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Beta-lactamase.
OS Staphylococcus aureus.
OC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RX MEDLINE=9642275; PubMed=8825372; DOI=10.1006/plas.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RT "The staphylococcal insertion sequence IS257 is active.";
RL Plasmid 34:198-205(1995).
DR EMBL: U36912; AAB39957.1; -.
DR EMBL: U36911; AAB39956.1; -.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR008711; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,le-96;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKKYKADQAGRVGTYELDLSGKTIIESRPERPMMSTFKYLGCGLVLSRID 60
DB 24 HPEITVKKYKADQAGRVGTYELDLSGKTIIESRPERPMMSTFKYLGCGLVLSRID 83
QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 120
DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 143
QY 121 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDERDTMPVANAATLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDERDTMPVANAATLRKLLTGELLTLASRQ 203
QY 181 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 240
DB 204 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 263
QY 241 SOATMDERNROIABIGASLIKIM 263
DB 264 SOATMDERNROIABIGASLIKIM 286

RESULT 3
Q79CL6 PRELIMINARY: PRT: 286 AA.
ID 079CL6
AC 079CL6: 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase.
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobacterales;
OC Methylobacteriaceae; Methylobacillus.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Seberijski I.G., Vassil V.M., Tsygankov Y.D.;

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RT "Two new members of the BioB superfamily: cloning, sequencing and
RT expression of bioB genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum.";
RL Gene 175:15-22(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Seberijski I., Vassil V., Tsygankov Y.;
RT Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL: U31280; AAC44581.1; -.
DR HSSP; P00807; IACO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR008711; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2,le-96;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKKYKADQAGRVGTYELDLSGKTIIESRPERPMMSTFKYLGCGLVLSRID 60
DB 24 HPEITVKKYKADQAGRVGTYELDLSGKTIIESRPERPMMSTFKYLGCGLVLSRID 83
QY 61 AGOELGRIRHYSONDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 120
DB 84 AGOELGRIRHYSONDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGP 143
QY 121 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDERDTMPVANAATLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDERDTMPVANAATLRKLLTGELLTLASRQ 203
QY 181 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 240
DB 204 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITGG 263
QY 241 SOATMDERNROIABIGASLIKIM 263
DB 264 SOATMDERNROIABIGASLIKIM 286

RESULT 4
Q79DR3 PRELIMINARY: PRT: 286 AA.
ID 079DR3
AC 079DR3: 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name=bla; Synonyms=blaTEM-116;
OS Escherichia coli.
OC Plasmid pRP4, and Plasmid pCAPs.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breitling F., the EMBL/Genbank/DBJ databases.
RN Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RC PLASMID=pCAPs;
RX MEDLINE=98189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;

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RT "A positive selection vector for cloning of long polymerase chain
 RT reaction fragments based on a lethal mutant of the *crp* gene
 RT *Escherichia coli*."; and plasmid pCRF04, and plasmid pCRF14
 RL Anal. Biochem. 257:203-209 (1998).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX PubMed=15243036;
 RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
 RA Kim Y.H., Jeong B.C., Lee S.H.;
 RT "Molecular Characterization of Extended-Spectrum Beta-lactamases
 RT Produced by Clinical Isolates of *Klebsiella pneumoniae* and *Escherichia*
 RT *coli* from a Korean Nationwide Survey."; J.
 RL Clin. Microbiol. 42:2902-2906 (2004).
 DR EMBL; Y12694; CAAT4057.1; -;
 DR EMBL; AJ001614; CA04868.1; -;
 DR EMBL; AY425988; AAQ95605.1; -;
 DR HSSP; P00807; 1ALQ.
 DR GO; GO:0008800; F:beta-lactamase activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PS00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolyase; Plasmid; Signal.
 FT SIGNAL 1 23
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 1348; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2,1e-96;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYELDINSKILIESPPEEPFPMSTFKYLCGAVSRID 60
 DB 24 HPELVKVDADQAGRVGYELDINSKILIESPPEEPFPMSTFKYLCGAVSRID 83
 QY 61 AGQELGRIRHYSQNDIVYSPVTEKHLIDGMYRELCSAATMSNTNANLLTTIGSP 120
 DB 84 AGQELGRIRHYSQNDIVYSPVTEKHLIDGMYRELCSAATMSNTNANLLTTIGSP 143
 QY 121 KELTAFLNMGDHYRLDRMEPELNEAIPNDRDITTPVAMATTLAKLTGELLTLASRQ 180
 DB 144 KELTAFLNMGDHYRLDRMEPELNEAIPNDRDITTPVAMATTLAKLTGELLTLASRQ 203
 QY 181 QIIDMEADKVAQPLIRSAIPAGWFIADKSGAGGERSGIIAALGPDGPRSRIVYITTG 240
 DB 204 QIIDMEADKVAQPLIRSAIPAGWFIADKSGAGGERSGIIAALGPDGPRSRIVYITTG 263
 QY 241 SQATMDERRROIAETGASLIKIM 263
 DB 264 SQATMDERRROIAETGASLIKIM 286

RESULT 5
 BLAT_ECOLI STANDARD; PRT; 286 AA.
 AC P62593; P00810; Q47313;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3)
 DE (TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6)
 DE (IRT-4) (Penicillinase).
 GN Name=bla;
 GN Name=bla;
 GN Name=blaT-3;
 GN Name=blaT-4;
 GN Name=blaT-5;
 GN Name=blaT-6;
 GN Name=blaT-6;

OS *Escherichia coli*.
 OG Plasmid R1 (R7268), Plasmid IncFII R100, Plasmid R6K, Plasmid pUD16,
 OG Plasmid pCRF04, and plasmid pCRF14
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=562;
 RN (1)
 RP SEQUENCE FROM N.A. (TEM-1).
 RC PLASMID-R1 (R7268); TRANSPOSON-Tn3;
 RX MEDLINE=79012484; PubMed=358200;
 RA Sutcliffe J.G.;
 RT "Nucleotide sequence of the ampicillin resistance gene of *Escherichia*
 RT *coli* plasmid pBR322."; J.
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3737-3741 (1978).
 RN (2)
 RP SEQUENCE FROM N.A. (TEM-1).
 RC PLASMID-R1 (R7268); TRANSPOSON-Tn3;
 RX MEDLINE=80002802; PubMed=383387;
 RA Sutcliffe J.G.;
 RT "Complete nucleotide sequence of the *Escherichia coli* plasmid
 RT pBR322."; J.
 RL Cold Spring Harb. Symp. Quant. Biol. 43:77-90 (1979).
 RN (3)
 RP SEQUENCE FROM N.A. (TEM-1).
 RC PLASMID-INCII R100;
 RX MEDLINE=86319522; PubMed=3019092; DOI=10.1016/0065-227X(86)90018-3;
 RA Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;
 RT "DNA replication of the resistance plasmid R100 and its control."; J.
 RL Adv. Biophys. 21:115-133 (1986).
 RN (4)
 RP SEQUENCE OF 24-286 (TEM-2).
 RC PLASMID-R6K; TRANSPOSON-Tn1;
 RX MEDLINE=79012483; PubMed=358199;
 RA Ambler R.P., Scott G.K.;
 RT "Partial amino acid sequence of penicillinase coded by *Escherichia*
 RT *coli* plasmid R6K."; J.
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3732-3736 (1978).
 RN (5)
 RP SEQUENCE FROM N.A. (TEM-3).
 RA Sougakoff W., Goussard S., Courvalin P.;
 RT "The TEM-3 beta-lactamase, which hydrolyzes broad-spectrum
 RT cephalosporins, is derived from the TEM-2 penicillinase by two amino
 RT acid substitutions."; J.
 RL FEMS Microbiol. Lett. 56:343-348 (1988).
 RN (6)
 RP SEQUENCE FROM N.A. (TEM-3).
 RC PLASMID-pCRF04;
 RX MEDLINE=93062798; PubMed=1331747;
 RA Mabilat C., Lourenco-Vital J., Goussard S., Courvalin P.;
 RT "A new example of physical linkage between Tn1 and Tn21: the
 RT antibiotic multiple-resistance region of plasmid pCRF04 encoding
 RT extended-spectrum beta-lactamase TEM-3."; J.
 RL Mol. Gen. Genet. 235:113-121 (1992).
 RN (7)
 RP SEQUENCE FROM N.A. (TEM-4 AND TEM-5).
 RC STRAIN-CH86134; PLASMID-pCRF04, and pUD16;
 RX MEDLINE=89378760; PubMed=2550326; DOI=10.1016/0378-1119(89)90236-9;
 RA Sougakoff W., Petit A., Goussard S., Sirot D., Bure A., Courvalin P.;
 RT "Characterization of the plasmid genes blaT-4 and blaT-5 which encode
 RT the broad-spectrum beta-lactamases TEM-4 and TEM-5 in
 RT enterobacteriaceae."; J.
 RL Gene 78:339-348 (1989).
 RN (8)
 RP SEQUENCE FROM N.A. (TEM-6).
 RC STRAIN-HB251;
 RX MEDLINE=9216702; PubMed=165171;
 RA Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courvalin P.;
 RT "An ISI-like element is responsible for high-level synthesis of
 RT extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae."; J.
 RL J. Gen. Microbiol. 137:2681-2687 (1991).
 RN (9)
 RP SEQUENCE FROM N.A. (TEM-8; TEM-16 AND TEM-24).
 RX MEDLINE=93037315; PubMed=1416873;

RA Chanal C., Poupart M.C., Sirot D., Labia R., Sirot J., Cluzel R.;
 RT "Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase
 RL genes.";
 RN Antimicrob. Agents Chemother. 36:1817-1820 (1992).
 (10)
 RP SEQUENCE OF 24-286 (IRT-4).
 RC STRAIN=PEY;
 RX MEDLINE=94333751; PubMed=8056282; DOI=10.1016/0378-1097(94)00186-3;
 RA Brun T., Peduzzi J., Canica M.M., Paul G., Nevot P., Barchelemy M.,
 Labia R.;
 RT "Characterization and amino acid sequence of IRT-4, a novel TEM-type
 RT enzyme with a decreased susceptibility to beta-lactamase inhibitors.";
 RL FEMS Microbiol. Lett. 120:111-117 (1994).
 (11)
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF TEM-1.
 RX MEDLINE=92183921; PubMed=1544485; DOI=10.1016/0014-5793(92)80232-6;
 RA Uelisch C., Lefant P., Masson J.-M., Samama J.-P.;
 RT "Beta-lactamase TEM1 of E. coli. Crystal structure determination at
 RT 2.5-A resolution.";
 RL FEBS Lett. 299:135-142 (1992).
 (12)
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF TEM-1.
 RX MEDLINE=93361453; PubMed=8356032;
 RA Uelisch C., Mourey L., Masson J.-M., Samama J.-P.;
 RT "Crystal structure of Escherichia coli TEM1 beta-lactamase at 1.8-A
 RT resolution.";
 RL Proteins 16:364-383 (1993).
 (13)
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF TEM-1 COMPLEXED WITH BLIP.
 RX MEDLINE=96186252; PubMed=8605632;
 RA Struykacka N.C.J., Jensen S.E., Alzari P.M., James M.N.G.;
 RT "A potent new mode of beta-lactamase inhibition revealed by the 1.7 A
 RT X-ray crystallographic structure of the TEM-1-BLIP complex.";
 RL Nat. Struct. Biol. 3:290-297 (1996).
 (14)
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF TEM-1.
 RX MEDLINE=98153145; PubMed=9485412; DOI=10.1021/b1972501b;
 RA Maveyraud L., Pratt R.F., Samama J.-P.;
 RT "Crystal structure of an acylation transition-state analog of the TEM-
 RT 1 beta-lactamase. Mechanistic implications for class A beta-
 RT lactamases.";
 RL Biochemistry 37:2622-2628 (1998).
 (15)
 RP X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF TEM-1.
 RX MEDLINE=99352177; PubMed=10423234; DOI=10.1021/b1990758z;
 RA Swaren P., Golemi D., Cabantous S., Bulchev A., Maveyraud L.,
 Mobashery S., Samama J.-P.;
 RT "X-ray structure of the Asn276asp variant of the Escherichia coli TEM-
 RT 1 beta-lactamase: direct observation of electrostatic modulation in
 RT resistance to inactivation by clavulanic acid.";
 RL Biochemistry 38:9570-9576 (1999).
 -I- FUNCTION: TEM-type are the most prevalent beta-lactamases in
 enterobacteria; they hydrolyze the beta-lactam bond in susceptible
 beta-lactam antibiotics, thus conferring resistance to penicillins
 and cephalosporins. TEM-3 and TEM-5 are capable of hydrolyzing
 cefotaxime and ceftazidime. TEM-5 is capable of hydrolyzing
 ceftazidime. TEM-6 is capable of hydrolyzing ceftazidime and
 aztreonam. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly
 active against ceftazidime. IRT-4 shows resistance to beta-
 lactamase inhibitors.
 -I- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 amino acid.
 -I- BIOTECHNOLOGY: This protein is used as a marker in many commonly
 used cloning vectors, such as pBR322 and the pUC series.
 -I- MISCELLANEOUS: The beta-lactamase present on pBR322 was cloned
 from plasmid R1 (R7268).
 -I- SIMILARITY: Belongs to the class-A beta-lactamase family.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J01749; AA59737.1; -
 DR EMBL: V00613; CA23886.1; -
 DR EMBL: X64523; CAA45828.1; -
 DR EMBL: X57972; CAA41038.1; -
 DR EMBL: X65252; CAA46344.1; -
 DR EMBL: X65253; CAA46345.1; -
 DR EMBL: X65254; CAA46346.1; -
 DR EMBL: U89928; AAB64386.1; -
 DR EMBL: U66885; AAC48875.1; -
 DR PIR: A93821; PNECP.
 DR PIR: S30113; S30113.
 DR PDB: 1AXB; X-ray; -
 DR PDB: 1B75; X-ray; -
 DR PDB: 1BTL; X-ray; -
 DR PDB: 1CK3; X-ray; -
 DR PDB: 1BRM; X-ray; -
 DR PDB: 1ERO; X-ray; -
 DR PDB: 1ERQ; X-ray; -
 DR PDB: 1RSU; X-ray; -
 DR PDB: 1FCG; X-ray; -
 DR PDB: 1OTD; X-ray; -
 DR PDB: 1OTG; X-ray; -
 DR PDB: 1UVJ; X-ray; -
 DR PDB: 1JWP; X-ray; -
 DR PDB: 1JWV; X-ray; -
 DR PDB: 1JWZ; X-ray; -
 DR PDB: 1LHY; X-ray; -
 DR PDB: 1L10; X-ray; -
 DR PDB: 1L19; X-ray; -
 DR PDB: 1NXY; X-ray; -
 DR PDB: 1NYO; X-ray; -
 DR PDB: 1NYI; X-ray; -
 DR PDB: 1TEM; X-ray; -
 DR PDB: 1XPB; X-ray; -
 Query Match 99.6%; Score 1343; DB 1; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5; 1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HPELVKVKQADQGAQVGYIELDNGKILLESFPERPPMSTFVLLCGAVLSRID 60
 DB 24 HPELVKVKQADQGAQVGYIELDNGKILLESFPERPPMSTFVLLCGAVLSRID 83
 QY 61 AGQELGRRIRYQNDLYEYSPYTEKHLTDGMYRELCSAITMSDNTAAVLLTTIGSP 120
 DB 84 AGQELGRRIRYQNDLYEYSPYTEKHLTDGMYRELCSAITMSDNTAAVLLTTIGSP 143
 QY 121 KELTAFLLNMGDHYTRLDWPEPELNEAIPNDERDTTPVMAATTLRKLLTGELLTLASRQ 180
 DB 144 KELTAFLLNMGDHYTRLDWPEPELNEAIPNDERDTTPVMAATTLRKLLTGELLTLASRQ 203
 QY 191 QLIDMEADKVAQPLRLRSALPAWGFADKSGAGERSGIIAALGDPKPSRIVVITYTG 240
 DB 204 QLIDMEADKVAQPLRLRSALPAWGFADKSGAGERSGIIAALGDPKPSRIVVITYTG 263
 QY 241 SQATDERNRQIAETGASLTKHW 263
 DB 264 SQATDERNRQIAETGASLTKHW 286
 RESULT 6
 BLAT_SALT
 ID BLAT_SALT STANDARD: PRT; 286 AA.
 AC P62594; P00810; Q47313;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Beta-lactamase TEM precursor (EC 3.5.2.6) (Penicillinase).
 GN Name=bla; OrderedLocusNames=Hcm1.216;
 OS Salmoneella typhi.

OG Plasmid pHC1.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OK NCBI_taxid=601;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parthill J., Dougan G., James K.D., Thomson M.R., Pickard D., Main J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutterell B.G., Simmons M., Skellon J., Stevens K.,
 RA Whitehead S., Whitehead K.M., Skellon J., Stevens K.,
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhimurium CT18.";
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: TEM-type are the most prevalent beta-lactamases in
 CC enterobacteria; they hydrolyze the beta-lactam bond in susceptible
 CC beta-lactam antibiotics, thus conferring resistance to penicillins
 CC and cephalosporins (By similarity).
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2O) = a substituted beta-
 CC amino acid.
 CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AL513383; CAD09800.1; -
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Antibiotic resistance; Complete proteome; Hydrolase; Plasmid; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 286 Beta-lactamase TEM.
 FT ACT_SITE 68 68 Acyl-ester intermediate (By similarity).
 FT ACT_SITE 166 166 Proton acceptor (By similarity).
 FT SITE 232 234 Substrate binding (By similarity).
 FT DISULFID 75 121 By similarity.
 SO SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 1; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5,1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPETLVKQADBDQAGAVGYEILDNSGKILSFRRPFRPMSTFVLLCGAVLSRD 60
 DB HPEITLVKQADBDQAGAVGYEILDNSGKILSFRRPFRPMSTFVLLCGAVLSRD 83
 QY 61 AGQEQIGRIHYSDNLYEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
 DB AGQEQIGRIHYSDNLYEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFLLNMGDHYTRLDWPEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
 DB KELTAFLLNMGDHYTRLDWPEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFLLNMGDHYTRLDWPEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 DB QLIIDMEADKVAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVYITGG 240
 QY 204 QLIIDMEADKVAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVYITGG 263
 DB 241 SOATWDERNRQIAEIGASLIKIM 263
 DB 264 SOATWDERNRQIAEIGASLIKIM 286

RESULT 7
 ID Q6A253 PRELIMINARY; PRT; 286 AA.
 AC Q6A253;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE Beta-lactamase TEM precursor (EC 3.5.2.6).
 GN Name=blatEM1; ORFNames=pl056.57c;
 OS Haemophilus influenzae.
 OG Plasmid ICBH1056.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 CC Pasteurellaceae; Haemophilus.
 OK NCBI_taxid=727;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Moth-Zain Z.;
 RA "Molecular biology of plasmid encoded resistance in *Haemophilus*
 RT influenzae.";
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Crook D.W.;
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ627386; CAF29065.1; -
 DR GO; GO:0008800; F:beta-lactamase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Hydrolase; Plasmid; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 24 286 beta-lactamase.
 SO SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5,1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPETLVKQADBDQAGAVGYEILDNSGKILSFRRPFRPMSTFVLLCGAVLSRD 60
 DB HPEITLVKQADBDQAGAVGYEILDNSGKILSFRRPFRPMSTFVLLCGAVLSRD 83
 QY 61 AGQEQIGRIHYSDNLYEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
 DB AGQEQIGRIHYSDNLYEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
 QY 121 KELTAFLLNMGDHYTRLDWPEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
 DB KELTAFLLNMGDHYTRLDWPEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFLLNMGDHYTRLDWPEPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
 DB QLIIDMEADKVAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVYITGG 240
 QY 204 QLIIDMEADKVAGPLLRALPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVYITGG 263
 DB 241 SOATWDERNRQIAEIGASLIKIM 263
 DB 264 SOATWDERNRQIAEIGASLIKIM 286

RESULT 8
 O6LBN9
 ID O6LBN9 PRELIMINARY; PRT; 286 AA.
 AC O6LBN9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Penicillinase TEM-1.
 GN Name=bla(tem-1A); Synonyms=bla(tem-1B);

OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 CX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91323733; PubMed=1650734; DOI=10.1016/0378-1119(91)90540-R;
 RA Goussard S., Courvalin P.;
 RT "Sequence of the genes blaT-1B and blaT-2."
 RL Gene 102:71-73(1991).
 DR EMBL; X54604; CAA38428.1; -.
 DR EMBL; X54607; CAA38430.1; -.
 DR HSSP; P00807; IALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIEIDLSGKILSFRRPPEPMPMSTFVLLCGAVLSRID 60
 DB 24 HPELVKVKADQDQAGVGYIEIDLSGKILSFRRPPEPMPMSTFVLLCGAVLSRID 83
 QY 61 AGQQLGRRHYSONDLYEVPVTEKHLTDGTVRELCSAATMSDNTAANLLTTTGGP 120
 DB 84 AGQQLGRRHYSONDLYEVPVTEKHLTDGTVRELCSAATMSDNTAANLLTTTGGP 143
 QY 121 KELTAFLLNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 144 KELTAFLLNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
 QY 181 QLIDMMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYTTG 240
 DB 204 QLIDMMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYTTG 263
 QY 241 SOATMDERNROIARIGASLIKHW 263
 DB 264 SOATMDERNROIARIGASLIKHW 286

RESULT 9

ID Q6LCV6 PRELIMINARY; PRT; 286 AA.
 AC Q6LCV6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 CX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GC1-182;
 RX MEDLINE=99225589; PubMed=10208798; DOI=10.1006/mcpr.1998.0216;
 RA Dillon J.R., Li H., Yeung K.-H., Aman T.A.;
 RT "A PCR assay for discriminating Neisseria gonorrhoeae beta-lactamase-producing plasmids."
 RL Mol. Cell. Probes 13:89-92(1999).
 RP SEQUENCE FROM N.A.
 RC STRAIN=GC1-182;
 RX MEDLINE=20079289; PubMed=10610817; DOI=10.1006/plas.1999.1431;
 RA Pagotto F., Aman A.T., Ng L.K., Yeung K.H., Bretz M., Dillon J.A.;
 RT "Sequence analysis of the family of penicillinase-producing plasmids from Neisseria gonorrhoeae.";

RL Plasmid 43:24-34(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GC1-182;
 RX MEDLINE=20156387; PubMed=10689182; DOI=10.1016/S0378-1119(99)00557-0;
 RA Pagotto F.J., Salimnia H., Totten P.A., Dillon J.R.;
 RT "Stable shuttle vectors for Neisseria gonorrhoeae, Haemophilus spp. and other bacteria based on a single origin of replication."
 RL Gene 244:13-19(2000).
 DR EMBL; U20374; AAB40517.1; -.
 DR HSSP; P00807; IALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Plasmid.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIEIDLSGKILSFRRPPEPMPMSTFVLLCGAVLSRID 60
 DB 24 HPELVKVKADQDQAGVGYIEIDLSGKILSFRRPPEPMPMSTFVLLCGAVLSRID 83
 QY 61 AGQQLGRRHYSONDLYEVPVTEKHLTDGTVRELCSAATMSDNTAANLLTTTGGP 120
 DB 84 AGQQLGRRHYSONDLYEVPVTEKHLTDGTVRELCSAATMSDNTAANLLTTTGGP 143
 QY 121 KELTAFLLNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 144 KELTAFLLNMGDHYTRLDRWPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
 QY 181 QLIDMMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYTTG 240
 DB 204 QLIDMMEADKYAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDGKPSRIIVYTTG 263
 QY 241 SOATMDERNROIARIGASLIKHW 263
 DB 264 SOATMDERNROIARIGASLIKHW 286

RESULT 10

ID Q6TMH1 PRELIMINARY; PRT; 286 AA.
 AC Q6TMH1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Name=blatEM-1.
 GN Streptococcus pneumoniae.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcaceae.
 CX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SR001;
 RA Ding Y., Huang Z.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY392531; AAC94057.1; -.
 DR HSSP; P00807; IALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;

Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPREPERPMSSTPKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPREPERPMSSTPKVLLCGAVLSRD 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELLTLASRQ 203
QY 181 OLIDMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAEIGASLIRKM 263
DB 264 SOATWDERNRQIAEIGASLIRKM 286

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RESULT 11

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ID 06W9J1 PRELIMINARY; PRT; 286 AA.
AC 06W9J1.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE TEM-1 beta-lactamase.
GN Name=blatEM-1;
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RA Cagno J., Katz S.E.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302260; AAQ73497.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

```

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPREPERPMSSTPKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPREPERPMSSTPKVLLCGAVLSRD 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELLTLASRQ 203
QY 181 OLIDMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAEIGASLIRKM 263
DB 264 SOATWDERNRQIAEIGASLIRKM 286

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RESULT 12

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ID 06WRX2 PRELIMINARY; PRT; 286 AA.
AC 06WRX2.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-lactamase TEM-1.
GN Name=blatEM-1;
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CP4;
RA Cagno J., Katz S.E.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271827; AAQ02307.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

```

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5.1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPREPERPMSSTPKVLLCGAVLSRD 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPREPERPMSSTPKVLLCGAVLSRD 83
QY 61 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRIHSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDRTTMAPAAATTIRKLLTGELLTLASRQ 203
QY 181 OLIDMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAGPLIRSLPAGWFIADKSGAGERSGRII AALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAEIGASLIRKM 263
DB 264 SOATWDERNRQIAEIGASLIRKM 286

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RESULT 13

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ID 06WZD4 PRELIMINARY; PRT; 286 AA.
AC 06WZD4.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Beta-lactamase TEM-1.
GN Name=blatEM-1;
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H240;
RA Huang Z., Chen Y., Mao P., Wu J., Wu L., Shan H., Shen J.;
RL Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.
[2]

```


RP SEQUENCE FROM N.A.
 RC STRAIN-1-43; Chen C.-H., Wu M.-H., Chu W.-C., Huang C.-W.;
 RA Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AY263331; AAP20891.1; -
 DR EMBL; AY560328; AAS68104.1; -
 DR HSSP; P00807; IALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5, 1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKDAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHSQNDLYEYSPVTEKHLTDGWTRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGQQLGRRIHSQNDLYEYSPVTEKHLTDGWTRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILNMGDHVTRLDRWPEPELNEAIPNDRDPTVPAVATTLRKLLTGELLTLASRQ 180
 DB 144 KEITAFILNMGDHVTRLDRWPEPELNEAIPNDRDPTVPAVATTLRKLLTGELLTLASRQ 203
 QY 181 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAIGPDGKPSRIIVITYTTG 240
 DB 204 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAIGPDGKPSRIIVITYTTG 263
 QY 241 SQATMDERNROIARIGASLIRKM 263
 DB 264 SQATMDERNROIARIGASLIRKM 286

RESULT 14
 ID Q7B3X5 PRELIMINARY; PRT; 286 AA.
 AC Q7B3X5;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE BLATEM1.
 GN Name=blATEM1;
 OS Citrobacter freundii.
 OG Plasmid pCTX-M3.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Citrobacter.
 CX NCBI_TaxID=546;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Gojebiewski M., Zienkiewicz M., Adamczyk M., Kern-Zdanowicz I.,
 RA Ceglowski P.;
 RL Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF550415; AAN87698.1; -
 DR HSSP; P00807; IALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;
 Best Local Similarity 99.2%; Pred. No. 5, 1e-96;
 Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HPELVKVKDAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60

DB 24 HPELVKVKDAEDQAGRVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHSQNDLYEYSPVTEKHLTDGWTRELCSAATMSDNTAANLLTTIGCP 120
 DB 84 AGQQLGRRIHSQNDLYEYSPVTEKHLTDGWTRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KEITAFILNMGDHVTRLDRWPEPELNEAIPNDRDPTVPAVATTLRKLLTGELLTLASRQ 180
 DB 144 KEITAFILNMGDHVTRLDRWPEPELNEAIPNDRDPTVPAVATTLRKLLTGELLTLASRQ 203
 QY 181 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAIGPDGKPSRIIVITYTTG 240
 DB 204 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGSGRGIITAAIGPDGKPSRIIVITYTTG 263
 QY 241 SQATMDERNROIARIGASLIRKM 263
 DB 264 SQATMDERNROIARIGASLIRKM 286

RESULT 15
 ID Q7B899 PRELIMINARY; PRT; 286 AA.
 AC Q7B899;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE TEM beta-lactamase TEM-1H.
 DE (Beta-lactamase TEM-1H).
 GN Name=bla; Synonyms=blATEM-1b, blATEM1H;
 OS Klebsiella pneumoniae.
 OG Plasmid pJHCW1, Plasmid pRM760, Plasmid E3, and Plasmid pKpn99-1029.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Klebsiella.
 CX NCBI_TaxID=573;
 RN [1]
 RA SEQUENCE FROM N.A.
 RC PLASMID=pJHCW1;
 RC MEDLINE=22270945; PubMed=12384346;
 RA Sarno R., McGilivray G., Sheratt D.J., Actis L.A., Tolmashy M.E.;
 RT "Complete nucleotide sequence of Klebsiella pneumoniae multiresistance
 RT plasmid pJHCW1.";
 RL Antimicrob. Agents Chemother. 46:3422-3427(2002).
 RN [2]
 RA SEQUENCE FROM N.A.
 RC PLASMID=pJHCW1;
 RA Tolmashy M.E.;
 RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RA SEQUENCE FROM N.A.
 RC PLASMID=pRM760;
 RA Partridge S.R., Hall R.M.;
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RA SEQUENCE FROM N.A.
 RC PLASMID=E3;
 RA Chen Y., Zhou W., Yu Y.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RA SEQUENCE FROM N.A.
 RC STRAIN=kpn99-1029; PLASMID=pKpn99-1029;
 RA Xiong Z., Zhu D., Wang F., Zhang Y.;
 RT "Study on the encoding gene of extended-spectrum beta-lactamases in a
 RT Klebsiella pneumoniae isolate.";
 RL Zhongguo Kang Sheng Su Za Zhi 28:96-100(2003).
 RN [6]
 RA SEQUENCE FROM N.A.
 RX PubMed=14613957;
 RA Nelson R.C., Segal H., Elieha B.G.;
 RT "Outer membrane protein alterations and blATEM-1 variants: their role
 RT in beta-lactam resistance in Klebsiella pneumoniae.";
 RL J. Antimicrob. Chemother. 52:999-903(2003).
 DR EMBL; AF479774; AAL93144.1; -

DR EMBL; AY123253; AAR91458.1; -;
DR EMBL; AF309824; AAG4772.1; -;
DR EMBL; AY293072; AAP43782.1; -;
DR EMBL; AY394610; AAQ96920.1; -;
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31515 MW; BB678943BB18934B CRC64;

Query Match 99.6%; Score 1343; DB 2; Length 286;

Best Local Similarity 99.2%; Pred.No. 5.1e-96;
Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMMSTFKVLLCGAVLSRID 60
|||
Db 24 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMMSTFKVLLCGAVLSRID 83
|||
QY 61 AGQEQIGRRIHYSQNDLVEYSPVTEKHLLDQMTVRELCSAATWMSDNTANILLTTIGGP 120
|||
Db 84 AGQEQIGRRIHYSQNDLVEYSPVTEKHLLDQMTVRELCSAATWMSDNTANILLTTIGGP 143
|||
QY 121 KEITAFLLNMGDHTRLDRMEPELNEAIPNDERDITMPVAMATTUKLLTGEILTLASRQ 180
|||
Db 144 KEITAFLLNMGDHTRLDRMEPELNEAIPNDERDITMPVAMATTUKLLTGEILTLASRQ 203
|||
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVITYTTG 240
|||
Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVITYTTG 263
|||
QY 241 SQATMDERNRQIAEIGASLIKKW 263
|||
Db 264 SQATMDERNRQIAEIGASLIKKW 286
|||

Search completed: June 10, 2005, 10:56:59
Job time : 90.1097 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 19.1791 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2

Perfect score: 1348

Sequence: 1 HPETLVKVDADQAGARVG.....TWDERNRQIAETGASLIRKW 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	286	2 TS1301	beta-lactamase (EC
2	1348	100.0	286	2 S47061	beta-lactamase (EC
3	1348	100.0	286	4 S41975	beta-lactamase (EC
4	1343	99.6	286	1 PNECP	beta-lactamase (EC
5	1343	99.6	286	4 I40905	beta-lactamase (EC
6	1330	98.7	286	2 S60312	extended spectrum
7	1329	98.6	286	2 S30113	beta-lactamase (EC
8	1323	98.1	286	2 S60310	extended spectrum
9	1321	98.0	286	2 S60311	beta-lactamase (EC
10	1317	97.7	286	2 J01546	Bla protein - Salim
11	936	69.4	265	2 S00464	beta-lactamase (EC
12	934	69.3	286	2 S16146	beta-lactamase (EC
13	934	69.3	286	2 A60679	beta-lactamase (EC
14	930	69.0	265	2 S02434	beta-lactamase (EC
15	930	69.0	286	1 A44998	beta-lactamase (EC
16	927	68.8	286	2 A37200	beta-lactamase (EC
17	926	68.7	286	2 A60632	beta-lactamase (EC
18	923	68.5	265	2 A60448	beta-lactamase (EC
19	901.5	66.9	287	1 A44996	beta-lactamase (EC
20	891	66.1	279	1 A24469	beta-lactamase (EC
21	866	64.2	286	1 A44958	beta-lactamase (EC
22	665	49.3	298	2 A41381	beta-lactamase (EC
23	527.5	39.1	288	2 J01136	beta-lactamase (EC
24	527.5	39.1	304	2 A35001	beta-lactamase (EC
25	524	38.9	105	2 UC2566	Bla protein - pseu
26	523.5	38.8	304	2 A49789	beta-lactamase (EC
27	517.5	38.4	288	2 J50755	beta-lactamase (EC
28	516.5	38.3	281	2 D95395	probable Beta lact
29	509.5	37.8	293	2 S04649	beta-lactamase (EC

30	509	37.8	276	2 JH0268	beta-lactamase (EC
31	503.5	37.4	263	2 A54543	beta-lactamase (EC
32	502.5	37.3	291	2 S42075	beta-lactamase (EC
33	493.5	36.6	302	2 S36188	beta-lactamase (EC
34	492.5	36.5	294	2 S16553	beta-lactamase (EC
35	489.5	36.5	306	1 B45822	beta-lactamase (EC
36	489.5	36.3	306	2 G69674	beta-lactamase (EC
37	488.5	36.2	306	2 S47330	penicillinase - Ba
38	482	35.8	291	2 JP0074	beta-lactamase (EC
39	480.5	35.6	305	2 A61156	beta-lactamase (EC
40	480.5	35.6	305	2 A57002	beta-lactamase (EC
41	480.5	35.6	305	2 A60680	beta-lactamase (EC
42	478	35.5	314	2 S06967	beta-lactamase (EC
43	472	35.0	263	2 S23929	beta-lactamase (EC
44	468.5	34.8	294	2 S19006	beta-lactamase (EC
45	464.5	34.5	306	2 S03167	beta-lactamase (EC

ALIGNMENTS

```

RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C1:Species: Schizosaccharomyces pombe
C1:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C1:Accession: TS1301
R1:WACH, A.; BRACHAT, A.; ALBERTSSEUT, C.; REBISCHUNG, C.; PHILIPSEN, P.
Yeast 13, 1065-1075, 1997
A1:Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharom
A1:Reference number: 209587
A1:Accession: TS1301
A1>Status: preliminary; translated from GB/EMBL/DBJ
A1:Molecule type: DNA
A1:Residues: 1-286 <MAC>
A1:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C1:Genetics:
A1:Gene: bla
C1:Superfamily: beta-lactamase I
C1:Keywords: hydrolase

Query Match      100.0%; Score 1348; DB 2; Length 286;
Best local similarity 100.0%; Pred. No. 1.2e-105;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPETLVKVDADQAGARVGYLELDNSGKTIESTRPERFPWMTFPKYLICGAVLSRID 60
DB      24 HPETLVKVDADQAGARVGYLELDNSGKTIESTRPERFPWMTFPKYLICGAVLSRID 83

QY      61 AGOBLGRRIHYSQNDLYEYSPYTEKHLTDGWTVELCSAATMTSDNTAANLLTTIGSP 120
DB      84 AGOBLGRRIHYSQNDLYEYSPYTEKHLTDGWTVELCSAATMTSDNTAANLLTTIGSP 143

QY      121 KELTAFINMGDHYTRLRWEPBELNEAIPNDERDITMPVAMATTIRKLLTGELITLASRQ 180
DB      144 KELTAFINMGDHYTRLRWEPBELNEAIPNDERDITMPVAMATTIRKLLTGELITLASRQ 203

QY      181 QIIDWMEADKVAGPIRLSALPAGWFIADKSGAGERGSGIIALGPDGKPSRIIVITYTTG 240
DB      204 QIIDWMEADKVAGPIRLSALPAGWFIADKSGAGERGSGIIALGPDGKPSRIIVITYTTG 263

QY      241 SQTMDERNRQIAETGASLIRKW 263
DB      264 SQTMDERNRQIAETGASLIRKW 286

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C1:Species: Phage phi-X174
C1:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C1:Accession: S47061
R1:Henrich, B.; Schmidtberger, B.

```

submitted to the EMBL Data Library, July 1994

A:Description: A variant of phix174 gene B-based positive selection vectors with enhance

A:Reference number: S47060

A:Accession: S47061

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <HEN>

A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase

Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.2e-105;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPEITLVKVDADDOUGARVGYIELDNGSKILIESFRPERPFPMSTFKYLTCGAVLSRD 60
DB 24 HPEITLVKVDADDOUGARVGYIELDNGSKILIESFRPERPFPMSTFKYLTCGAVLSRD 83
OY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGCP 120
DB 84 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGCP 143
OY 121 KELTAFILNMGDHVTRLDRWBELENEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWBELENEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 203
OY 181 OLIDWMDKAVGAPLLRSALPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIVIYTTG 240
DB 204 OLIDWMDKAVGAPLLRSALPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIVIYTTG 263
OY 241 SOATMDERRROIAEIGASLIRKM 263
DB 264 SOATMDERRROIAEIGASLIRKM 286

RESULT 3

S41975 beta-lactamase (EC 3.5.2.6) precursor - synthetic

C:Species: synthetic

C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000

C:Accession: S41975

R:Kaschner, K.H.; Montolín, L.; Kern, H.; Thulke, M.; Schutz, G.

Gene 148, 67-70, 1994

A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar

A:Reference number: A51991; MUID:95011660; PMID:7926839

A:Accession: S41975

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-286 <KAB>

A:Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623

A:Note: submitted to the EMBL Data Library, December 1993

C:Keywords: hydrolase

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.2e-105;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPEITLVKVDADDOUGARVGYIELDNGSKILIESFRPERPFPMSTFKYLTCGAVLSRD 60
DB 24 HPEITLVKVDADDOUGARVGYIELDNGSKILIESFRPERPFPMSTFKYLTCGAVLSRD 83
OY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGCP 120
DB 84 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGCP 143
OY 121 KELTAFILNMGDHVTRLDRWBELENEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWBELENEAIPNDRDITTPVAMATTIRKLLTGELTLASRQ 203
OY 181 OLIDWMDKAVGAPLLRSALPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIVIYTTG 240
DB 204 OLIDWMDKAVGAPLLRSALPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIVIYTTG 263

OY 241 SOATMDERRROIAEIGASLIRKM 263
DB 264 SOATMDERRROIAEIGASLIRKM 286

RESULT 4

PNECP

beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmid

N:Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase

C:Species: Escherichia coli

C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005

R:Suciliffe, J.G.

Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978

A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid

A:Reference number: A93821; MUID:79012484; PMID:358200

A:Accession: A93821

A:Molecule type: DNA

A:Residues: 1-286 <STU>

A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:g43710; PIDN:CAA23886.1; P

A:Experimental source: plasmid pBR322

R:Ambler, R.P.; Scott, G.K.

Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978

A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid

A:Reference number: A93820; MUID:79012483; PMID:358199

A:Accession: A93820

A:Molecule type: protein

A:Residues: 24-36, 'K', 38-286 <AMB>

A:Experimental source: plasmid R6K

R:Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.

J. Bacteriol. 172, 3040-3050, 1990

A:Title: The kil-kor region of broad-host-range plasmid RK2: nucleotide sequence, polype

A:Reference number: A35387; MUID:90264294; PMID:2160936

A:Accession: A35387

A:Molecule type: DNA

A:Residues: 182-286 <KOR>

A:Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1; PID:g152522

A:Experimental source: PK2

R:Gonsard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.

J. Gen. Microbiol. 137, 2681-2687, 1991

A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum

A:Accession: S24415

A:Residues: 524415; MUID:92166702; PMID:1665171

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>

A:Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817

A:Experimental source: ISI-like blaT-6 DNA

R:Suciliffe, J.G.

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.

A:Reference number: A90923; MUID:80002802; PMID:383387

A:Accession: A90923

A:Status: annotation

A:Contents: annotation

C:Comment: Like most penicillinases from gram-negative bacteria, this enzyme, coded by a

C:Genetics:

A:Superfamily: Beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-286/Product: beta-lactamase #status experimental <MAT>

F:68/Active site: Ser #status predicted

F:75-121/Disulfide bonds: #status predicted

Query Match 99.6%; Score 1343; DB 1; Length 286;
Best Local Similarity 99.2%; Pred. No. 3.1e-105;
Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITLVKVDADDOUGARVGYIELDNGSKILIESFRPERPFPMSTFKYLTCGAVLSRD 60
DB 24 HPEITLVKVDADDOUGARVGYIELDNGSKILIESFRPERPFPMSTFKYLTCGAVLSRD 83
OY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGCP 120

|||||
Db AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 143
Qy 121 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 240
Db 204 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 263
Qy 241 SOATMDERRROJAEIGASLIRKM 263
Db 264 SOATMDERRROJAEIGASLIRKM 286

RESULT 5
140905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A>Note: Cloning vector pCC1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*
C>Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: 140905
R:Taylor, J.; Stearman, R.S.; Uratani, B.B.
A>Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A:Reference number: 140904; PMID:93361581; PMID:7689234
A:Accession: 140905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RBS>
A:Cross-references: EMBL:U21228; NID:g885956; PDB:AAA70411.1; PID:g885958
C:Keywords: hydrolase

Query Match 99.6%; Score 1343; DB 4; Length 286;
Best Local Similarity 99.2%; Pred. No. 3, 1e-105;
Matches 261; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 83
Qy 61 AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 143
Qy 121 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 240
Db 204 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 263
Qy 241 SOATMDERRROJAEIGASLIRKM 263
Db 264 SOATMDERRROJAEIGASLIRKM 286

RESULT 6
S60312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanal, C.; Poupert, M.C.; Strot, D.; Labia, R.; Strot, J.; Clusel, R.
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; PMID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:g296955; PDB:CAA46346.1; PID:g296956
C:Superfamily: beta-lactamase I

Query Match 98.7%; Score 1330; DB 2; Length 286;
Best Local Similarity 98.1%; Pred. No. 3, 8e-104;
Matches 258; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 83
Qy 61 AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 143
Qy 121 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 240
Db 204 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 263
Qy 241 SOATMDERRROJAEIGASLIRKM 263
Db 264 SOATMDERRROJAEIGASLIRKM 286

RESULT 7
S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFP04

C:Species: *Klebsiella pneumoniae*
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Jul-2004
C:Accession: S30113
R:Mabliat, C.; Lourenco-Vital, J.; Gousard, S.; Courvalin, P.
A:Title: A new example of physical linkage between *Tn1* and *Tn21*: the antibiotic multiple.
A:Reference number: S30112; PMID:93062798; PMID:1331747
A:Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PDB:CAA45828.1; PID:g43798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.6%; Score 1329; DB 2; Length 286;
Best Local Similarity 98.1%; Pred. No. 4, 6e-104;
Matches 258; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKVDADQAGARVGYELDLNSGKILSPRPBRPFPMSTFKVLLCGAVLSRD 83
Qy 61 AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVYSPVTEKHLTDGNTVRELCSAATMTSDNTANILLTTIGSP 143
Qy 121 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWBEPELNEAIPNDRDRTTMPVAMATTIRKLLTGELITLASRQ 203
Qy 181 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 240
Db 204 QUIDMWEADKVAQPLIRSLPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVYITTTG 263
Qy 241 SOATMDERRROJAEIGASLIRKM 263
Db 264 SOATMDERRROJAEIGASLIRKM 286

C:Date: 31-Dec-1998 #sequence_reviston 31-Dec-1998 #text_change 18-Jun-1993
C:Accession: S00464
R:Barthelemy, M.; Peduzzi, J.; Labia, R.
R:Biochem. J. 251, 73-79, 1988
A:Title: Complete amino acid sequence of p43-plasmid-mediated *pir*-2 beta-lactamase (SH)
A:Reference number: S00464; MUID:88268817; PMID:3260490
A:Accession: S00464
A:Molecule type: protein
A:Residues: 1-265 <BAR>
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.4%; Score 936; DB 2; Length 265;
Best Local Similarity 67.9%; Pred. No. 4,2e-71;
Matches 178; Conservative 38; Mismatches 46; Indels 0; Gaps 0;

QY 2 PETLVKVVADADQIGARVGYTELDNSGKILSPRPSPRPSPMTFKVLCGATLSRIDA 61
D 2 POPLEQILDSQQLSGRGVMTLMDLASSRTLTAMPADRFPMSTFKVLCGATLSRIDA 61
QY 62 GOEOLGRIRHISQNDLVESPVTEKHLIDGNTVRELCSAATITMSDNTFANLLTTIGSPK 121
D 62 GDEQLERKIRHQDDLVYSPVSEKHLADGNTVRELCSAATITMSDNTFANLLTTIGSPK 121
QY 122 ELTAFILNMGDHYVRLDRWEPELNEAIPNDERDITTPVMAVTTLRKLLTGELTTASRQ 181
D 122 GLTAFILRQIGDNTVRLDRWEPELNEAIPNDERDITTPVMAVTTLRKLLTGELTTASRQ 181
QY 182 LIDWMEADKVAQPLIRSLTPAGWFIADKSGGERSKRIITALLPDDGSPSIVITYTGS 241
D 182 LIDWMEADKVAQPLIRSLTPAGWFIADKSGGERSKRIITALLPDDGSPSIVITYTGS 241
QY 242 QATDERNRQAFIAGASLIKHM 263
D 242 PASHAERNQQLAGIGALIEHM 263

RESULT 12
S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence_reviston 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146; A35395; S18767
R:Podbielski, A.; Schoening, J.; Melzer, B.; Warnatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SH)
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817; NID:G43795; PIDN:CAA37813.1; PID:G43796
A:Experimental source: plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A35395; MUID:90264317; PMID:2160941
A:Accession: A35395
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LER>
A:Cross-references: GB:X52115; NID:G46988; PIDN:CAA44025.1; PID:G46990
A:Experimental source: plasmid BMH77
C:Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.3%; Score 934; DB 2; Length 286;
Best Local Similarity 67.6%; Pred. No. 6.8e-71;

Matches	177;	Conservative	38;	Mismatches	47;	Indels	0;	Gaps	0;
QY	2	PELVKVVADADQIGARVGYIELDINSKILIESFPBERPMMSTFKVLLCGAVLSRIDA	61						
Db	23	POPLEIQIKOSSESQSLSGRVGMIEMDLASGRITLTAWPADERFPMMSTFKVLLCGAVLARVDA	82						
QY	62	GOEOLGRRIHYSQNDLVVSPYTEKGLTDGMVTRRLCSAATMSDNTANLLTTGGPK	121						
Db	83	GDEOLERRKHTRQODLVVSPVSEKHLADGMVTRVGLCSAATMSDNSAANLLATVGGPA	142						
QY	122	ELTAFILHMGGHVTRLDMEPELNEAIPNDERDITMPVMAATTLRLTGLGELLTLASROO	181						
Db	143	GLTAFILRIGDNYTRLDMEPELNEALDGDARDITTPASMAATTLRLTSLQSLSARSQRO	202						
QY	182	LIDWMEADKVAQPLIRLSALPAGWFIADKSGAGERSGRIIALLGPDGKPSRIVITYTGS	241						
Db	203	LLQWNVDDRVAVGPIRLRSVLPAGWFIADKXTGASERGARGIVALLGPNNKARIVIVYLRDT	262						
QY	242	QATDERRKROIAETGASLITKHW	263						
Db	263	PASMAERNQOITAGIGALLIERH	284						

RESULT 13

A60679
beta-lactamase (EC 3.5.2.6) SHV-2 precursor - *Salmonella typhimurium* plasmid pHT11

C:Species: *Salmonella typhimurium*
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C:Accession: A60679

R:Garbary-Chenon, A.; Godard, V.; Labie, R.; Nicot, J.C.
Anticarb. Agents Chemother. 34, 1444-1446, 1990
A:Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A:Reference number: A60679; MUID:90351141; PMID:2201259
A:Accession: A60679
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <GAR>
A:Cross-references: GB:L47119; NID:g972890; PID:AAA75015.1; PID:g972891
C:Genetics:
A:Genome: plasmid
C:Superfamily: Beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase
F:1-21/Domain: signal sequence #status predicted <SIG>

Query Match 69.3%; Score 934; DB 2; Length 286;
Best Local Similarity 67.6%; Pred. No. 6.8e-71;
Matches 177; Conservative 38; Mismatches 47; Indels 0; Gaps 0;

QY	2	PELVKVVADADQIGARVGYIELDINSKILIESFPBERPMMSTFKVLLCGAVLSRIDA	61
Db	23	POPLEIQIKOSSESQSLSGRVGMIEMDLASGRITLTAWPADERFPMMSTFKVLLCGAVLARVDA	82
QY	62	GOEOLGRRIHYSQNDLVVSPYTEKGLTDGMVTRRLCSAATMSDNTANLLTTGGPK	121
Db	83	GDEOLERRKHTRQODLVVSPVSEKHLADGMVTRVGLCSAATMSDNSAANLLATVGGPA	142
QY	122	ELTAFILHMGGHVTRLDMEPELNEAIPNDERDITMPVMAATTLRLTGLGELLTLASROO	181
Db	143	GLTAFILRIGDNYTRLDMEPELNEALDGDARDITTPASMAATTLRLTSLQSLSARSQRO	202
QY	182	LIDWMEADKVAQPLIRLSALPAGWFIADKSGAGERSGRIIALLGPDGKPSRIVITYTGS	241
Db	203	LLQWNVDDRVAVGPIRLRSVLPAGWFIADKXTGASERGARGIVALLGPNNKARIVIVYLRDT	262
QY	242	QATDERRKROIAETGASLITKHW	263
Db	263	PASMAERNQOITAGIGALLIERH	284

RESULT 14

S02434
beta-lactamase (EC 3.5.2.6) SHV-2 - *Escherichia coli*
Species: *Escherichia coli*

C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993

C/Accession: S02434

R/Batch: Lemay, M.; Peduzzi, J.; Yaghlane, H.B.; Labie, R.

R/EBBS Lett. 231, 217-220, 1988

A/Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hyd

A/Reference number: S02434; MUID:88196385; PMID:3129309

A/Accession: S02434

A/Molecule type: protein

A/Residues: 1-265 <BAR>

C/Superfamily: beta-lactamase I

C/Keywords: antibiotic resistance; hydrolase

Query Match 69.0%; Score 930; DB 2; Length 265;

Best Local Similarity 67.6%; Pred. No. 1.3e-70;

Matches 177; Conservative 38; Mismatches 47; Indels 0; Gaps 0;

QY 2 PETLVKVDADQGLGARVGYIELDINSKILSPFPERFPMSTFKYLCCGAVLSRIDA 61

DB 2 PQLPQIKLSQSGLGRVGMIEMLASGRITLAWRADRFPMSTFKYVLCGAVLARVDA 61

QY 62 GQQLGRRIHSONDIYVSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGPK 121

DB 62 GDEQLERKIHQQDLVDYSPVSEKHLADGNTVRELCSAATMSDNTANLLTTAVGSPA 121

QY 122 ELTAFILHMGDHTVRLDRWEPELNEAIPNDERDTMPVAMATTLRKLTGELLTLASRQ 181

DB 122 GLTAFILRQIGDNTVRLDRWEPELNEALPGDARDTTTPASMAATTLRKLTLSQRLSARSQ 181

QY 182 LIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRTIALGPDGKPSRIIVITGTS 241

DB 182 LLOQWVDDRVAGPLIRSVLPAGWFIADKSGAGERSGRTIALGPNNAERIVIVITLNDT 241

QY 242 QATMDERRROTAETGASLIKEM 263

DB 242 PASMAERNQOLAGIGALLIEHW 263

RESULT 15

A44998 beta-lactamase (EC 3.5.2.6) SHV-2 - Klebsiella ozaenae plasmid pBB60

C/Species: Klebsiella ozaenae

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C/Accession: A44998; S12703

R/Huletaky, A.; Couture, F.; Lavesque, R.C.

Antimicrob. Agents Chemother. 34, 1725-1732, 1990

A/Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.

A/Reference number: A44998; MUID:91136192; PMID:2285285

A/Accession: A44998

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-286 <HUU>

A/Cross-references: UNIPROT:P14558; GB:M95179; NID:G150488; PIDN:AAA5526.1; PID:G150489

R/Podbielski, A.; Melzer, B.

Nucleic Acids Res. 18, 4916, 1990

A/Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2))

A/Reference number: S12703; MUID:90370479; PMID:2395654

A/Accession: S12703

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-286 <POD>

A/Cross-references: EMBL:X53433; NID:G43789; PIDN:CAA37524.1; PID:G43790

C/Genetics:

A/Genome: plasmid

C/Superfamily: beta-lactamase I

C/Keywords: antibiotic resistance; hydrolase

Query Match 69.0%; Score 930; DB 1; Length 286;

Best Local Similarity 67.6%; Pred. No. 1.5e-70;

Matches 177; Conservative 38; Mismatches 47; Indels 0; Gaps 0;

QY 2 PETLVKVDADQGLGARVGYIELDINSKILSPFPERFPMSTFKYLCCGAVLSRIDA 61

DB 23 PQLPQIKLSQSGLGRVGMIEMLASGRITLAWRADRFPMSTFKYVLCGAVLARVDA 82

QY 62 GQQLGRRIHSONDIYVSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGPK 121

DB 83 GDEQLERKIHQQDLVDYSPVSEKHLADGNTVRELCSAATMSDNTANLLTTAVGSPA 142

QY 122 ELTAFILHMGDHTVRLDRWEPELNEAIPNDERDTMPVAMATTLRKLTGELLTLASRQ 181

DB 143 GLTAFILRQIGDNTVRLDRWEPELNEALPGDARDTTTPASMAATTLRKLTLSQRLSARSQ 202

QY 182 LIDWMEADKVAGPLIRSLPAGWFIADKSGAGERSGRTIALGPDGKPSRIIVITGTS 241

DB 203 LLOQWVDDRVAGPLIRSVLPAGWFIADKSGAGERSGRTIALGPNNAERIVIVITLNDT 262

QY 242 QATMDERRROTAETGASLIKEM 263

DB 263 PASMAERNQOLAGIGALLIEHW 284

Search completed: June 10, 2005, 10:58:44
Job time : 20.1791 secs

XX (PANO-) PANORAMA RES INC.
 PA
 XX
 PI Balint RF, Her J;
 XX
 DR WPI; 2001-451857/48.
 DR N-PSDB; AAD10411.
 XX

PT Interaction-dependent enzyme association systems for detecting
 PT interactions between two or three polypeptides, especially in human
 PT therapeutics, diagnostics or prognostics, comprise circularly permuted
 PT proteins.
 XX
 PS
 XX

Claim 38; Fig 2; 104pp; English.

XX The invention relates to new interaction-dependent enzyme association
 CC (IDBA) systems that comprise a fusion sequence that encodes for a
 CC circularly permuted, interaction-activated proteins that reassemble to
 CC form functionally reconstituted marker proteins which produce a
 CC detectable signal upon the association of two oligopeptides, or upon
 CC simultaneous association of two oligopeptides with a third oligopeptide.
 CC The marker protein is preferably a type A beta-lactamase, especially TEM-
 CC 1 beta-lactamase of *Escherichia coli*. The oligopeptide is a member of a
 CC proteome library selected from single chain antibody Fv fragment library,
 CC an antibody light chain variable region library and a peptide library
 CC displayed within thioredoxin. The IDBA systems are useful for detecting
 CC and identifying interactions between intracellular as well as
 CC extracellular proteins, particularly between two or three polypeptides.
 CC The systems are also useful in selecting with a single marker protein the
 CC incorporation of multiple genetic traits in a host cell. In particular,
 CC the systems are useful in many applications in human therapeutics,
 CC diagnostics and prognostics, as well as in high-throughput screening
 CC systems for the discovery and validation of pharmaceutical targets and
 CC drugs. Prior systems (e.g. B. coli Dimer Detection System, yeast two-
 CC hybrid system or Selective Infective Phage System) require multiple steps
 CC between interaction and phenotype, which cause severe loss of efficiency
 CC due to high false positive and false negative rates. The present system
 CC is capable of simultaneous detection of multiple interactions between
 CC extra-cellular as well as intracellular proteins in a high throughput
 CC format. The circularly permuted marker proteins comprising interaction-
 CC dependent enzymes find use in cell-based sensors for activation or
 CC inhibition of metabolic or signal transduction pathways, in high-
 CC throughput mapping of pair-wise protein-protein interactions within and
 CC between the proteomes of cells, tissues and pathogenic organisms, and in
 CC cell-based screens for high-throughput selection of inhibitors of any
 CC protein-protein interaction. The present sequence is *Escherichia coli*
 CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
 CC lactamase is a product of ampicillin resistance gene. The enzyme has two
 CC domains, alpha-omega and mu
 CC
 XX

Sequence 263 AA;

Query Match 100.0%; Score 1348; DB 4; Length 263;

Best Local Similarity 100.0%; Pred. No. 1.8e-132; Mismatches 0; Indels 0; Gaps 0;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 QY 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 DB 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 QY 121 KETLAPFLNMGDHYTRLDREPELNEALPNDERDTTMMVAATTKLLTSELTLARQ 180
 121 KETLAPFLNMGDHYTRLDREPELNEALPNDERDTTMMVAATTKLLTSELTLARQ 180
 DB 121 KETLAPFLNMGDHYTRLDREPELNEALPNDERDTTMMVAATTKLLTSELTLARQ 180
 121 KETLAPFLNMGDHYTRLDREPELNEALPNDERDTTMMVAATTKLLTSELTLARQ 180
 QY 181 QLIDMMEADKAGPLLRSGALPAGWFIADSGAGERSGIIAALGPDGKPSRIIVITYTG 240
 181 QLIDMMEADKAGPLLRSGALPAGWFIADSGAGERSGIIAALGPDGKPSRIIVITYTG 240
 DB 181 QLIDMMEADKAGPLLRSGALPAGWFIADSGAGERSGIIAALGPDGKPSRIIVITYTG 240
 181 QLIDMMEADKAGPLLRSGALPAGWFIADSGAGERSGIIAALGPDGKPSRIIVITYTG 240
 QY 241 SOATMDERNROIATIGASLIRHW 263
 241 SOATMDERNROIATIGASLIRHW 263

DB 241 SOATMDERNROIATIGASLIRHW 263

RESULT 2
 AAB36692
 ID AAB36692 standard; protein; 263 AA.

XX AAB36692;
 AC
 XX 15-MAR-2001 (first entry)
 DT
 XX
 XX
 DE
 XX
 XX
 XX

Escherichia coli mature TEM-1 beta-lactamase protein sequence.

Interaction-activated protein; beta-lactamase; protein interaction.

Escherichia coli.

MO200071702-A1.

30-NOV-2000.

16-MAR-2000; 2000WO-US007108.

25-MAY-1999; 99US-0135926P.

13-JAN-2000; 2000US-0175968P.

(PANO-) PANORAMA RES INC.

Balint RF, Her J;

WPI; 2001-032034/04.

N-PSDB; AAC90773.

PT Novel fragment complementation system to identify interactions between
 PT polypeptides comprises fragment pairs having first and second members
 PT that reassemble into a marker protein which has a directly detectable
 PT signal.

Disclousure; Fig 2; 94pp; English.

XX The present invention describes a fragment complementation system (I)
 CC which comprises a first oligopeptide (OP1) containing an N-terminal
 CC fragment with a C-terminal break point and a second oligopeptide (OP2)
 CC comprising a C-terminal with a N-terminal breakpoint, in which the C and
 CC N terminal fragments are both derived from a marker protein (MP) and
 CC reassemble to form a functionally reconstituted MP. Methods from the
 CC present invention are used for monitoring the occurrence of protein-
 CC protein interactions in a sample, identifying oligopeptide interactions
 CC between two different proteomes, identifying epitopes that bind to an
 CC immunoglobulin (Ig) variable region, for identifying interactions between
 CC an extracellular domain of a transmembrane protein and a polypeptide, for
 CC high-throughput identification of compounds that inhibit phosphorylation-
 CC regulated signal transducers, forming a enzyme complementation system for
 CC selecting simultaneous incorporation of multiple genetic elements into a
 CC host cell and for activating a beta-lactam derivative of an antitumor
 CC compound in a host who is in need of it. The present sequence represents
 CC the *Escherichia coli* mature TEM-1 beta-lactamase, which is used in the
 CC exemplification of the present invention
 CC
 XX

Sequence 263 AA;

Query Match 100.0%; Score 1348; DB 4; Length 263;

Best Local Similarity 100.0%; Pred. No. 1.8e-132; Mismatches 0; Indels 0; Gaps 0;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 1 HPEITLVKVKADADOLGARVGYIEIDLSNGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 QY 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 DB 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
 61 AGOQOLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120

QY 121 KETLAFPHNMGDHTRLDRWPELNEAI PNDERDTMPVAAVTLTKLLTGELLTLASRQ 180
 DB 121 KETLAFPHNMGDHTRLDRWPELNEAI PNDERDTMPVAAVTLTKLLTGELLTLASRQ 180
 QY 181 QLIMWMDKVGAGPLNSALPAGWFIADKSGAGSGRGIIAALGPDGKPSRIVVIYTTG 240
 DB 181 QLIMWMDKVGAGPLNSALPAGWFIADKSGAGSGRGIIAALGPDGKPSRIVVIYTTG 240
 QY 241 SQATMDERNROIARIIGASLIRGW 263
 DB 241 SQATMDERNROIARIIGASLIRGW 263

RESULT 3
 ADJ67709
 ID ADJ67709 standard; protein; 263 AA.
 XX
 AC ADJ67709;
 DT 20-MAY-2004 (first entry)
 DE Escherichia coli TEM-1 beta-lactamase.
 XX
 KW fragment complementation system; marker protein;
 KW multiple genetic element incorporation; antibiotic resistance;
 KW beta-lactam derivative activation; anti-tumour compound;
 KW functional reassembly; protein-protein interaction; proteome interaction;
 KW immunoglobulin variable region; immune cell protein; CD40;
 KW phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KW enzyme.
 XX
 OS Escherichia coli.
 PN US2004036317-A1.
 XX
 PD 26-FEB-2004.
 PF 22-SEP-2003; 2003US-00668778.
 XX
 PR 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175968P.
 PR 13-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIOIS INC.
 XX
 PI Balint RF, Her J;
 XX
 DR WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47pp; English.
 XX
 CC The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and reassemble
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneously incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;

CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)
 CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 XX
 SQ Sequence 263 AA;
 XX
 Query Match 100.0%; Score 1348; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1,8e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQLGARVGYIEIDLNSGKILSFRRPBERPPMNSTFRVLLCGAVLSRID 60
 DB 1 HPEITLVKVDADQLGARVGYIEIDLNSGKILSFRRPBERPPMNSTFRVLLCGAVLSRID 60
 QY 61 AGQKQLGRRIHYSONDIVESPVTEKHLTDGMTVREICSAITMSDNTAAVLLTTIGSP 120
 DB 61 AGQKQLGRRIHYSONDIVESPVTEKHLTDGMTVREICSAITMSDNTAAVLLTTIGSP 120
 QY 121 KETLAFPHNMGDHTRLDRWPELNEAI PNDERDTMPVAAVTLTKLLTGELLTLASRQ 180
 DB 121 KETLAFPHNMGDHTRLDRWPELNEAI PNDERDTMPVAAVTLTKLLTGELLTLASRQ 180
 QY 181 QLIMWMDKVGAGPLNSALPAGWFIADKSGAGSGRGIIAALGPDGKPSRIVVIYTTG 240
 DB 181 QLIMWMDKVGAGPLNSALPAGWFIADKSGAGSGRGIIAALGPDGKPSRIVVIYTTG 240
 QY 241 SQATMDERNROIARIIGASLIRGW 263
 DB 241 SQATMDERNROIARIIGASLIRGW 263

RESULT 4
 AAM16634
 ID AAM16634 standard; protein; 264 AA.
 XX
 AC AAM16634;
 DT 09-AUG-1997 (first entry)
 DE Beta-lactamase (including signal peptide).
 XX
 KW Gene directed enzyme prodnrg therapy; GDEPT;
 KW virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KW HIV, inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key
 FT Peptide
 FT /label= Sig_peptide
 XX
 PN MO9719180-A2.
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;

DR WPI; 1997-298117/27.
DR N-PSDB; AAT66736.

XX Molecular chimera for gene or virus directed enzyme prodng therapy -
PT useful for treatment of cancer, viral infection or inflammation.
XX

PS Example; Page 28; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
CC is the expression product of a molecular chimera, designated PCMV-BL
CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
CC intermediate/early promoter. Vectors consisting of a transcriptional
CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
CC enzyme prodng therapy. Expression of the beta-lactamase in a targeted
CC cell allows conversion of a prodng into an agent toxic to the cell for
CC treatment of cancer. Viral (e.g. HIV) infection or inflammation.
CC Secretion of the enzyme has the advantage of increasing neighbouring cell
CC kill
CC

XX Sequence 264 AA;

Query Match 100.0%; Score 1348; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 1.8e-132; Indels 0; Gaps 0;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIELDLSGKILSFREPERPMMSTFVLLCGAVLSRID 60
DB 2 HPELVKVKADQDQAGVGYIELDLSGKILSFREPERPMMSTFVLLCGAVLSRID 61
QY 61 AGGOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 62 AGGOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 121
QY 121 KELAPFLNMGDHYTRLDRMEPELNEALPNDERDTMPVAAVTLRKLLTSELTLASRQ 180
DB 122 KELAPFLNMGDHYTRLDRMEPELNEALPNDERDTMPVAAVTLRKLLTSELTLASRQ 181
QY 181 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGRGSGRIIALGPDGKPSRIIVITYTTG 240
DB 182 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGRGSGRIIALGPDGKPSRIIVITYTTG 241
QY 241 SQATMDERNRQIAEIGASLIRKW 263
DB 242 SQATMDERNRQIAEIGASLIRKW 264

RESULT 5

AAW16680
ID AAW16680 standard; protein; 264 AA.

XX AAW16680;

XX 13-AUG-1997 (first entry)

XX Intracellularly-expressed beta-lactamase.

XX Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
KW virus directed enzyme prodng therapy; VDEPT; lung cancer;
KW beta-lactamase; PCMV-delBL.

XX Escherichia coli.

XX MO9719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Sethna PB;

XX WPI; 1997-298118/27.
DR N-PSDB; AAT70311.

XX DNA construct for gene-directed enzyme prodng therapy of lung cancer -
PT comprises lung- or neuroendocrine-specific promoter controlling
PT expression of prodng-converting enzyme.
XX

PS Example 811; Page 32-34; 53pp; English.

XX The intracellular form (AAW16680) of TEM beta-lactamase is expressed by
CC PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
CC sequence, minus the signal sequence, is placed under control of the
CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
CC lactamase constructs, placed under control of promoter/enhancer elements
CC of lung-associated protein or neuroendocrine marker protein genes, can be
CC used in novel chimeric molecules for use in prodng therapy of lung
CC cancer
CC

XX Sequence 264 AA;

Query Match 100.0%; Score 1348; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 1.8e-132; Indels 0; Gaps 0;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDQAGVGYIELDLSGKILSFREPERPMMSTFVLLCGAVLSRID 60
DB 2 HPELVKVKADQDQAGVGYIELDLSGKILSFREPERPMMSTFVLLCGAVLSRID 61
QY 61 AGGOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 62 AGGOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 121
QY 121 KELAPFLNMGDHYTRLDRMEPELNEALPNDERDTMPVAAVTLRKLLTSELTLASRQ 180
DB 122 KELAPFLNMGDHYTRLDRMEPELNEALPNDERDTMPVAAVTLRKLLTSELTLASRQ 181
QY 181 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGRGSGRIIALGPDGKPSRIIVITYTTG 240
DB 182 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGRGSGRIIALGPDGKPSRIIVITYTTG 241
QY 241 SQATMDERNRQIAEIGASLIRKW 263
DB 242 SQATMDERNRQIAEIGASLIRKW 264

RESULT 6

AAW16680
ID AAW16680 standard; protein; 264 AA.

XX AAW16680;

XX 10-MAR-2003 (revised)

XX 04-JUN-1993 (first entry)

XX Ampicillin resistance protein.
KW CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;
KW xenobiotics; circular; chimeric cytochrome P4501A1.

XX Homo sapiens.

XX US5180666-A.

XX 19-JAN-1993.

XX 27-JUN-1991; 91US-00721775.

XX 27-JUN-1991; 91US-00721775.

XX (UYMA-) UNIV WAYNE STATE.

XX States JC, Hines RN, Novak RF;

```

XX  WP1; 1993-052845/06.
DR  N-PSDB; AA036498.
XX
XX  In vitro method for testing mutagenicity of a chemical - by metabolising
PT  chemical cell line consisting of transformed fibroblasts having
PT  detectable cytochrome P450 mixed function oxidase activity and detecting
PT  gene damage.
XX
XX  Disclosure; Col 21-24; 24pp; English.
XX
XX  The expression constructs PRNH127 and PRNH155 contain identical sequences
CC  but were constructed using different strategies (see AA036498). The
CC  constructs comprise exons 2-7 of human CYP1A1 gene under the control of
CC  the inducible mouse metallothionein (MT-1) promoter. The constructs also
CC  contain an open reading frame in the opposite orientation to the
CC  cytochrome P450 exons. This ORF encodes ampicillin resistance. The
CC  constructs are suitable for transformation of human fibroblasts derived
CC  from the xeroderma pigmentosum group A. Cultures of the transformed
CC  fibroblasts can be used to test substances for mutagenicity. The presence
CC  of the inducible cytochrome P450 gene allows metabolism of the substance
CC  to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
CC  field.)
XX
SQ  Sequence 286 AA:

Query Match      100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 HPEITLVKTKDABDQAGAVGYIELDLSGKILLESFRPERPPMSTFVYLCAVLSRID 60
    |||||
DB  24 HPEITLVKTKDABDQAGAVGYIELDLSGKILLESFRPERPPMSTFVYLCAVLSRID 83
QY  61 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
    |||||
DB  84 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY  121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 180
    |||||
DB  144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 203
QY  181 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 240
    |||||
DB  204 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 263
QY  241 SOATMDERNROIABIGASLIRKM 263
    |||||
DB  264 SOATMDERNROIABIGASLIRKM 286
    |||||

RESULT 7
ID  AAR97619 standard; protein; 286 AA.
XX
XX  AAR97619;
XX
XX  20-AUG-1996 (first entry)
XX
XX  Secretory beta-lactamase.
XX
XX  Gene therapy; gene directed enzyme prodnug therapy; GDBPT;
KM  virus directed enzyme prodnug therapy; VDBPT; prodnug activation;
KM  cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;
KM  beta-lactamase; cephalosporin.
XX
XX  Synthetic.
XX
XX  WO9616179-A1.
XX
XX  30-MAY-1996.
XX
XX  20-NOV-1995; 95WO-GB002716.

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XX  18-NOV-1994; 94GB-00023367.
PR  (WELL ) WELLCOME FOUND LTD.
XX
XX  Dev IK, Moore JT, Ohmsted C;
PI  WP1; 1996-268615/27.
XX
XX  WP1; 1996-268615/27.
DR  N-PSDB; AAT29220.
XX
XX  Molecular chimera for use in enzyme gene therapy - is activated in a
PT  target cell to express a secretable enzyme which cleaves a prodnug
PT  outside the cell into a cytotoxic or cytostatic agent.
XX
XX  Example 3; Page 57-58; 73pp; English.
XX
XX  A secretory beta-lactamase (AAR97619) is expressed from DNA construct
CC  PCMW-BL (AAT29220), in which the beta-lactamase coding sequence is under
CC  the control of the intermediate/early cytomegalovirus promoter. Beta-
CC  lactamase delivery to mammalian cells confers sensitivity to
CC  cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations
CC  resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
CC  of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
CC  was increased upon i.t. injection of the secretory beta-lactamase DNA
CC  construct
XX
SQ  Sequence 286 AA:

Query Match      100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 HPEITLVKTKDABDQAGAVGYIELDLSGKILLESFRPERPPMSTFVYLCAVLSRID 60
    |||||
DB  24 HPEITLVKTKDABDQAGAVGYIELDLSGKILLESFRPERPPMSTFVYLCAVLSRID 83
QY  61 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
    |||||
DB  84 AGOBLGRRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY  121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 180
    |||||
DB  144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITTMVAMATTLRKLLTGELTLASRQ 203
QY  181 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 240
    |||||
DB  204 OLIDMEADKVAAGPLIRGALPAGWFIADKSGAGERSGIIIALGPDGKPSRIVIYTTG 263
QY  241 SOATMDERNROIABIGASLIRKM 263
    |||||
DB  264 SOATMDERNROIABIGASLIRKM 286
    |||||

RESULT 8
ID  AAR96423 standard; protein; 286 AA.
XX
XX  AAR96423;
XX
XX  25-MAR-2003 (revised)
XX  25-NOV-1996 (first entry)
XX
XX  Cytochrome P450 (CYP1A1 construct).
DB  cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KM  metabolism.
XX
XX  Homo sapiens.
XX
XX  US5525482-A.
XX
XX  11-JUN-1996.

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PF 15-NOV-1994; 94US-00339658.
 XX
 PR 27-JUN-1991; 91US-00721775.
 PR 09-DEC-1992; 92US-0090295.
 XX
 PA (UTWA-) UNIV WAYNE STATE.
 XX
 PI Hines RN, Novak RF, States JC;
 XX
 DR WPI: 1996-286397/29.
 N-PSDB; AAT30354.
 XX
 PT Testing chemicals for cytotoxicity to human by detecting gene damage -
 PT using recombinant fibroblasts transformed with cytochrome P450 gene under
 PT control of inducible promoter.
 XX
 PS Disclosure; Col 17-24; 26pp; English.
 XX
 CC The present sequence is encoded by a chimeric mouse metallothionein-
 CC cytochrome P450Ia1 (CYP1A1) expression construct. Two clones, PRNH127 and
 CC PRNH15, were isolated by different methods and which both had the same
 CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
 CC of humans to a chemical. The method comprises exposing human fibroblast
 CC cells normally not including any cytochrome P450 activity to potentially
 CC toxic chemicals. The cells having been transformed to express cytochrome
 CC P450, under the control of a controllable promoter through the CYP1A1
 CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
 CC intracellularly into a cytochrome metabolite by oxidation within the
 CC fibroblasts through the intracellular cytochrome P450 mixed function
 CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
 CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
 CC -MAR-2003 to correct PF field.)
 XX
 SQ Sequence 286 AA;

Query Match 100.0%; Score 1348; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQKDEPDGARGVYIEIDLSGKILSFREPERPMMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKQKDEPDGARGVYIEIDLSGKILSFREPERPMMSTFVLLCGAVLSRID 83
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 143
 QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIPNDEBDTTPVAVATTIRKLLTSELTLASRQ 180
 DB 144 KETLAFILNMGDHYTRLDRMEPELNEAIPNDEBDTTPVAVATTIRKLLTSELTLASRQ 203
 QY 181 QLTIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTTG 240
 DB 204 QLTIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTTG 263
 QY 241 SQATMDERNROIAGISGLIKHW 263
 DB 264 SQATMDERNROIAGISGLIKHW 286

RESULT 9
 AAM16635
 ID AAM16635 standard; protein; 286 AA.
 XX
 AC AAM16635;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (no signal peptide).
 XX
 KW Gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.

XX
 OS Escherichia coli.
 XX
 PN W09719180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmsted C;
 XX
 DR WPI: 1997-298117/27.
 N-PSDB; AAT66737.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodng therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 26; 38pp; English.

CC Escherichia coli beta-lactamase (AAM16635), lacking the signal peptide,
 CC is the expression product of a molecular chimera, designated PCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodng therapy. Intracellular expression of the beta-lactamase in
 CC a targetted cell allows conversion of a prodng into an agent toxic to
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or
 CC inflammation
 XX
 SQ Sequence 286 AA;

Query Match 100.0%; Score 1348; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQKDEPDGARGVYIEIDLSGKILSFREPERPMMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKQKDEPDGARGVYIEIDLSGKILSFREPERPMMSTFVLLCGAVLSRID 83
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 143
 QY 121 KETLAFILNMGDHYTRLDRMEPELNEAIPNDEBDTTPVAVATTIRKLLTSELTLASRQ 180
 DB 144 KETLAFILNMGDHYTRLDRMEPELNEAIPNDEBDTTPVAVATTIRKLLTSELTLASRQ 203
 QY 181 QLTIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTTG 240
 DB 204 QLTIMMEADKYAGPLRLSALPAGWFIADKSGAGRSRGITIALGPDGKPSRIVITYTTG 263
 QY 241 SQATMDERNROIAGISGLIKHW 263
 DB 264 SQATMDERNROIAGISGLIKHW 286

RESULT 10
 AAM18679
 ID AAM18679 standard; protein; 286 AA.
 XX
 AC AAM18679;
 XX
 DT 13-AUG-1997 (first entry)
 XX
 DE Secretory beta-lactamase.
 XX
 KW Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
 KW virus directed enzyme prodng therapy; VDEPT; lung cancer;
 KW beta-lactamase; PCMV-BL.

```
XX Escherichia coli.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Protein 24..286
XX /label= Sig_peptide
XX /label= Mat_protein
XX
XX WO9719183-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002846.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Sethna PB;
XX
XX WPI; 1997-298118/27.
XX
XX N-PSDB; AAT70309.
XX
XX DNA construct for gene-directed enzyme prodnrg therapy of lung cancer -
XX comprises lung- or neuroendocrine-specific promoter controlling
XX expression of prodrg-converting enzyme.
XX
XX Example 811; Page 26-27; 53pp; English.
XX
XX The secreted form (AA018679) of TEM beta-lactamase is expressed by PCMV-
XX BL (AA070309) in which a PCR-amplified beta-lactamase coding sequence is
XX placed under control of the intermediate/early promoter of
XX Cytomegalovirus. Secretory beta-lactamase constructs, placed under
XX control of promoter/enhancer elements of lung- associated protein or
XX neuroendocrine marker protein genes, can be used in novel chimaeric
XX molecules for use in prodrg therapy of lung cancer
XX
XX Sequence 286 AA:
SQ
Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKTKDABDQGAAGVGYIELDLSGKTIIESRPERPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKTKDABDQGAAGVGYIELDLSGKTIIESRPERPMMSTFVLLCGAVLSRID 83
QY 61 AGOGLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOGLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 240
DB 204 QLIDMMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 263
QY 241 SOATMDERNROIAGSLIKHW 263
DB 264 SOATMDERNROIAGSLIKHW 286
XX
XX RESULT 11
XX ID AAY08529 standard; protein; 286 AA.
XX AC AAY08529;
XX DT 03-AUG-1999 (first entry)
XX
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```
DE Vector pASK75 beta-1a protein.
XX
XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
XX tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
XX insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
XX allergy.
XX
XX Synthetic.
XX
XX WO9925866-A1.
XX
XX 27-MAY-1999.
XX
XX 11-NOV-1998; 98WO-FI000873.
XX
XX 14-NOV-1997; 97FI-00004235.
XX
XX (KORP/) Korpela M.
XX (KARP/) Karp M.
XX (KURIT/) Kurittu J.
XX
XX Korpela M, Karp M, Kurittu J;
XX
XX WPI; 1999-338015/28.
XX
XX N-PSDB; AAV72418.
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
XX
XX Disclosure; Page 47-48; 67pp; English.
XX
XX This invention describes a novel tetracycline assay that uses recombinant
XX prokaryotic cells comprising a luciferase gene under the transcriptional
XX control of a tetracycline repressor and tetracycline promoter and
XX involves the detection of luminescence emitted from the cells. The assay
XX can be used to distinguish tetracycline from other microbial agents. The
XX invention also describes a novel plasmid comprising either the luxCDABE
XX genes, a tetracycline repressor (Tetr) and a tetracycline promoter (TetA)
XX from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
XX and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
XX method can be used for the determination of tetracycline in a sample,
XX e.g. to study the dosage and penetration of the medicine. The method can
XX also be used to test cheese production, as cheese making bacteria are not
XX able to work in the presence of tetracycline. The method can also be used
XX to determine the presence or concentration of antibiotics in foodstuffs,
XX e.g. for allergic people. The present assay method does not rely on the
XX growth of microbes as do conventional tests, and so is much more rapid.
XX The present assay is also more sensitive, as even a small amount of
XX luminescence can be detected
XX
XX Sequence 286 AA:
SQ
Query Match 100.0%; Score 1348; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKTKDABDQGAAGVGYIELDLSGKTIIESRPERPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKTKDABDQGAAGVGYIELDLSGKTIIESRPERPMMSTFVLLCGAVLSRID 83
QY 61 AGOGLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOGLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 240
DB 204 QLIDMMEADKVAAGPLIRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYITG 263
QY 241 SOATMDERNROIAGSLIKHW 263
XX
```


Db 264 SOATMDERNROIAEIGASLIRKW 286

RESULT 12
AAB10442
ID AAB10442 standard; protein; 286 AA.
XX
AC AAB10442;
XX
DT 01-DEC-2000 (first entry)
XX
DE Expression vector pSEX15G2 bla protein.
XX
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
OS Synthetic.
XX
DE1900635-A1.
XX
PD 13-JUL-2000.
XX
PF 11-JAN-1999; 99DE-01000635.
XX
PR 11-JAN-1999; 99DE-01000635.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Breitling F, Poustka A, Moldenhauer G;
XX
DR WPI; 2000-499832/45.
XX
N-PSDB; AAA71430.
XX
PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
PS Claim 16; Fig 3; 22pp; German.
XX
CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX15G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
SQ Sequence 286 AA;
XX
Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 HPELTIVKXKADBDQAGAVGYIELDLSNGKILSRPBERPFWMTFVLLCGAVLSRID 60
OY |||||||
DB 61 AGOELGRIRIHNSQDVLVEYSPVTEKHLTDGWTVELCSAATWSDNPAANLLTTIGSP 120
OY |||||||
DB 84 AGOELGRIRIHNSQDVLVEYSPVTEKHLTDGWTVELCSAATWSDNPAANLLTTIGSP 143
OY |||||||
OY 121 KETLTAFLHMGDHTRLDRWEPELNEAIPNDERDTTTPVAAATTLKLLTGELTLTASRQ 180

Db 144 KETLTAFLHMGDHTRLDRWEPELNEAIPNDERDTTTPVAAATTLKLLTGELTLTASRQ 203
OY |||||||
OY 181 QLIDWMEADKVAGPLLSALPAGMFIADKSGAGRGSRGIIAALGPDKSPRIYVITYTG 240
DB 204 QLIDWMEADKVAGPLLSALPAGMFIADKSGAGRGSRGIIAALGPDKSPRIYVITYTG 263
OY 241 SOATMDERNROIAEIGASLIRKW 263
DB 264 SOATMDERNROIAEIGASLIRKW 286

RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.
XX
AC AAB10438;
XX
DT 01-DEC-2000 (first entry)
XX
DE Expression vector pSEX11L4 bla protein.
XX
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX
OS Synthetic.
XX
DE1900635-A1.
XX
PD 13-JUL-2000.
XX
PF 11-JAN-1999; 99DE-01000635.
XX
PR 11-JAN-1999; 99DE-01000635.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Breitling F, Poustka A, Moldenhauer G;
XX
DR WPI; 2000-499832/45.
XX
N-PSDB; AAA71428.
XX
PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
PS Claim 16; Fig 1; 22pp; German.
XX
CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the Neo-R
CC protein contained in the expression vector pSEX11L4 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
SQ Sequence 286 AA;
XX
Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADBDQAGAVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHYSQNDLVESPVTEKHLTDGMTVELCSAAITMSDNTAANLLTTTIGSP 120
 DB 84 AGQQLGRRIHYSQNDLVESPVTEKHLTDGMTVELCSAAITMSDNTAANLLTTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDREWEPELNEAIPNDERDTMPVAAATTLRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDREWEPELNEAIPNDERDTMPVAAATTLRKLLTGELTLASRQ 203
 QY 181 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSRGITAAIGPDGKPSRIVVIYTTG 240
 DB 204 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSRGITAAIGPDGKPSRIVVIYTTG 263
 QY 241 SOATMDERNRQIAEIGASLIRKM 263
 DB 264 SOATMDERNRQIAEIGASLIRKM 286

RESULT 14
 AAB10440
 ID AAB10440 standard; protein; 286 AA.
 AC AAB10440;
 XX
 XX 01-DEC-2000 (first entry)
 XX
 DE Expression vector pSEX11G2 bla protein.
 XX
 KM Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
 KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
 XX
 OS Synthetic.
 XX
 PN DE19900635-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 11-JAN-1999; 99DE-01000635.
 XX
 PR 11-JAN-1999; 99DE-01000635.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Breitling F, Poustka A, Moldenhauer G;
 XX
 DR WPI: 2000-499832/45.
 DR N-PSDB; AAA71429.
 XX
 PT Selecting monoclonal antibodies, by expressing them on the surface of
 PT hybridomas attached to antibody-binding protein, then reaction with
 PT antibody library.
 XX
 PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
 CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
 CC cells to produce antibody-producing hybridomas such that the antibodies
 CC are presented at the surface of the hybridomas by an antibody-binding
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The
 CC invention also describes antibody-binding proteins (I) that comprise a
 CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
 CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
 CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
 CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
 CC or CD52. The method is used to select Mab with specificity for particular
 CC antigens. Mab can be selected without separate culture of hybridomas, and
 CC selection can be made against many antigens in a library, optionally on
 CC the basis of strength of affinity for a particular antigen. Complex
 CC mixtures of hybridomas can be used for selection, reducing the time and
 CC cost involved in Mab selection. This sequence represents the bla protein

CC protein contained in the expression vector pSEX11G2 which contains the
 CC bla protein, Neo-R and protein G described in the method of the invention
 CC
 SQ Sequence 286 AA;
 Query Match 100.0%; Score 1348; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2e-132;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADBDQAGAVGYIELDLSNGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGQQLGRRIHYSQNDLVESPVTEKHLTDGMTVELCSAAITMSDNTAANLLTTTIGSP 120
 DB 84 AGQQLGRRIHYSQNDLVESPVTEKHLTDGMTVELCSAAITMSDNTAANLLTTTIGSP 143
 QY 121 KELTAFILNMGDHYTRLDREWEPELNEAIPNDERDTMPVAAATTLRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHYTRLDREWEPELNEAIPNDERDTMPVAAATTLRKLLTGELTLASRQ 203
 QY 181 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSRGITAAIGPDGKPSRIVVIYTTG 240
 DB 204 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSRGITAAIGPDGKPSRIVVIYTTG 263
 QY 241 SOATMDERNRQIAEIGASLIRKM 263
 DB 264 SOATMDERNRQIAEIGASLIRKM 286

RESULT 15
 AAB50898
 ID AAB50898 standard; protein; 286 AA.
 AC AAB50898;
 XX
 XX 20-MAR-2001 (first entry)
 XX
 DT Protein encoded by bla resistance marker of integration vector pLO12306.
 XX
 DE bla resistance marker; recombinant host cell; saccharification;
 XX fermentation; polysaccharase; oligosaccharide degradation; celz gene;
 KM glucanase; integration vector; pLO12306.
 XX
 OS Unidentified.
 XX
 PN WO200071729-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014773.
 XX
 PR 26-MAY-1999; 99US-0136376P.
 XX
 PA (UVFL) UNIV FLORIDA RES FOUND.
 XX
 PI Ingram LO, Zhou S;
 XX
 DR WPI: 2001-032043/04.
 DR N-PSDB; AAC91455.
 XX
 PT Recombinant host cells useful for producing polysaccharase for degrading
 PT oligosaccharides, comprises a first heterologous polynucleotide encoding
 PT polysaccharase under control of surrogate promoter.
 XX
 PS Disclosure; Page 82-83; 87pp; English.

CC The present sequence is given in a specification relating to a
 CC recombinant host cell suitable for simultaneous saccharification and
 CC fermentation. The host cell contains at least one heterologous
 CC polynucleotide encoding a polysaccharase under the transcriptional
 CC control of a surrogate promoter capable of increasing expression of the
 CC polysaccharase. The host cell also contains a second heterologous

CC polynucleotide encoding a secretory polypeptide to facilitate the
 CC secretion of the expressed polysaccharase. The recombinant host cell is
 CC useful for producing polysaccharase which is useful for enzymatically
 CC degrading oligosaccharides such as lignocellulose, hemicellulose,
 CC cellulose, pectin or their combinations, and fermenting the product to
 CC ethanol, by simultaneous saccharification and fermentation processes. The
 CC present sequence is encoded by an integration vector which was introduced
 CC into cells to generate recombinant host cells. The vector contains a
 CC surrogate promoter from *Zymomonas mobilis*, the *celZ* gene from *Erwinia*
 CC *chrysanthemi*, resistance markers *bla* and *tet*, and *Klebsiella oxytoca*
 CC target sequence

XX Sequence 286 AA;

Query Match 100.0%; Score 1348; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 2e-132;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPE TLVKKVKAEDQIGARVGYIELDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID	60
Db	24	HPE TLVKKVKAEDQIGARVGYIELDLNSGKILSFPRPERFPMWSTFKVLLCGAVLSRID	83
Qy	61	AGQEQLGRRIRYSQNDLVEYSPVTEKHLTDGWTYRELCSAAITMSDNTAANILLTTIGSP	120
Db	84	AGQEQLGRRIRYSQNDLVEYSPVTEKHLTDGWTYRELCSAAITMSDNTAANILLTTIGSP	143
Qy	121	KELTAFLHNMGDHYTRLDRMEPELNEAIPNDEBDTTPVAMATTLLRKLLTGELLTIASRQ	180
Db	144	KELTAFLHNMGDHYTRLDRMEPELNEAIPNDEBDTTPVAMATTLLRKLLTGELLTIASRQ	203
Qy	181	QLIDWMEADKYVAPLLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITYTTG	240
Db	204	QLIDWMEADKYVAPLLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIIVITYTTG	263
Qy	241	SOATMDERNROIARIIGASLIRHW	263
Db	264	SOATMDERNROIARIIGASLIRHW	286

Search completed: June 10, 2005, 10:49:09
 Job time : 103.972 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 26.9646 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2

Perfect score: 1348
Sequence: 1 HPEITLVKVDADQUGARVG.....TMDERNRQIAETGASLHKW 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1348	100.0	286	1	US-07-721-775A-2
2	1348	100.0	286	1	US-08-339-658-2
3	1348	100.0	286	3	US-09-263-933-7
4	1348	100.0	286	3	US-09-263-933-14
5	1348	100.0	286	3	US-09-263-933-21
6	1348	100.0	286	3	US-09-263-933-21
7	1348	100.0	286	3	US-09-263-933-21
8	1348	100.0	286	3	US-09-263-933-21
9	1348	100.0	286	4	US-09-919-901-14
10	1348	100.0	286	4	US-09-919-901-14
11	1348	100.0	286	4	US-09-919-901-21
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13	1348	100.0	286	4	US-09-919-901-21
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18	1348	100.0	286	4	US-09-919-901-21
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21	1348	100.0	286	4	US-09-919-901-21
22	1348	100.0	286	4	US-09-919-901-21
23	1348	100.0	286	4	US-09-919-901-21
24	1348	100.0	286	4	US-09-919-901-21
25	1348	100.0	286	4	US-09-919-901-21
26	1348	100.0	286	4	US-09-919-901-21
27	1348	100.0	286	4	US-09-919-901-21

28	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	1348	100.0	299	4	US-09-490-153-300	Sequence 285, App
30	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
31	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
32	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
33	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
34	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
35	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
36	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
37	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
38	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
39	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
40	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
41	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
42	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
43	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App
44	1348	100.0	299	4	US-09-490-153-300	Sequence 298, App
45	1348	100.0	299	4	US-09-490-153-300	Sequence 300, App

ALIGNMENTS

RESULT 1
US-07-721-775A-2

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:
APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:
ADDRESSER: Relating, Echington, Barnard, Perry & Milton

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07721,775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30, 955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-721-775A-2

Query Match 100.0%; Score 1348; DB 1; Length 286;
Best local similarity 100.0%; Pred. No. 5.2e-141;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQUGARVGITELDNGKILIESRPERPMMSTFKVLGAVLSRD 60
DB 24 HPEITLVKVDADQUGARVGITELDNGKILIESRPERPMMSTFKVLGAVLSRD 83

QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDERDTMPVAMATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDERDTMPVAMATTLRKLLTSELTLASRQ 203
QY 181 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROIAETIGASLIRHW 263
DB 264 SOATMDERNROIAETIGASLIRHW 286

RESULT 2
US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5525482
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5525482ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
; STREET: P. O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339, 658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 100.0%; Score 1348; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDERDTMPVAMATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDERDTMPVAMATTLRKLLTSELTLASRQ 203
QY 181 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROIAETIGASLIRHW 263
DB 264 SOATMDERNROIAETIGASLIRHW 286

RESULT 3
US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-7

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGIETLDLNSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGIETLDLNSGKILSFRRPFRPMSSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDERDTMPVAMATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDERDTMPVAMATTLRKLLTSELTLASRQ 203
QY 181 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATMDERNROIAETIGASLIRHW 263
DB 264 SOATMDERNROIAETIGASLIRHW 286

RESULT 4
US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A

;; CURRENT APPLICATION NUMBER: US/09/263,933
;; CURRENT FILING DATE: 1999-03-08
;; EARLIER APPLICATION NUMBER: 09/129,611
;; EARLIER FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGRVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRRIHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRRIHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHVTRLDRWEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFLLNMGDHVTRLDRWEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVVIYTTG 240
DB 204 QLIDWMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVVIYTTG 263
QY 241 SQATMDERNRQIAETGASLIRKM 263
DB 264 SQATMDERNRQIAETGASLIRKM 286

RESULT 5
US-09-263-933-21
;; Sequence 21, Application US/09263933
;; Patent No. 6280940
;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patrick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/263,933
;; CURRENT FILING DATE: 1999-03-08
;; EARLIER APPLICATION NUMBER: 09/129,611
;; EARLIER FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKADADQAGRVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGRVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRRIHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRRIHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHVTRLDRWEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 180

DB 144 KELTAFLLNMGDHVTRLDRWEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVVIYTTG 240
DB 204 QLIDWMEADKVAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVVIYTTG 263
QY 241 SQATMDERNRQIAETGASLIRKM 263
DB 264 SQATMDERNRQIAETGASLIRKM 286

RESULT 6
US-09-025-769B-265
;; Sequence 265, Application US/09025769B
;; Patent No. 6300064
;; GENERAL INFORMATION:
;; APPLICANT: Knappik, Achim
;; APPLICANT: Pack, Peter
;; APPLICANT: Ilag, Vic
;; APPLICANT: Ge, Liming
;; APPLICANT: Moroney, Simon
;; APPLICANT: Plueckthun, Andreas
;; TITLE OF INVENTION: Protein/(Poly)peptide libraries
;; NUMBER OF SEQUENCES: 373
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;; INFORMATION FOR SEQ ID NO: 265:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKADADQAGRVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGRVGYIELDLSGKILSFPRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRRIHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRRIHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHVTRLDRWEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFLLNMGDHVTRLDRWEPELNEALPNDERDITMPVAAATTLRKLLTGELLTLASRQ 203

QY 181 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIVYTTG 240
DB 204 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIVYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

RESULT 7

US-09-025-769B-362
; Sequence 362, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 1348; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXKADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKXKADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 203
QY 181 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIVYTTG 240

DB 204 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIVYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

RESULT 8

US-09-919-901-7
; Sequence 7, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2001-08-02
; PRIOR FILING DATE: 09/129,901
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXKADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKXKADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
DB 84 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGLLTLASRQ 203
QY 181 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIVYTTG 240
DB 204 OLIDMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVIVYTTG 263
QY 241 SOATWDERNRQIAETIGASLIRKM 263
DB 264 SOATWDERNRQIAETIGASLIRKM 286

RESULT 9

US-09-919-901-14
; Sequence 14, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAALTMSDNTAANLLTTTGGP 120
DB 84 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAALTMSDNTAANLLTTTGGP 143
QY 121 KELTAFILNMGDHYRLDRMEPELNEAIPNDRDRTTVPVAAATTIRKLLTGSELTLASRQ 180
DB 144 KELTAFILNMGDHYRLDRMEPELNEAIPNDRDRTTVPVAAATTIRKLLTGSELTLASRQ 203
QY 181 OLIDMEADKVAQPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAQPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAETGASLIKHW 263
DB 264 SOATWDERNRQIAETGASLIKHW 286

RESULT 10
US-09-919-901-21
Sequence 21, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAALTMSDNTAANLLTTTGGP 120
DB 84 AGQEQGRIRHYSQNDLYEVSPTVEKHLTDGTVRELCSAALTMSDNTAANLLTTTGGP 143
QY 121 KELTAFILNMGDHYRLDRMEPELNEAIPNDRDRTTVPVAAATTIRKLLTGSELTLASRQ 180
DB 144 KELTAFILNMGDHYRLDRMEPELNEAIPNDRDRTTVPVAAATTIRKLLTGSELTLASRQ 203
QY 181 OLIDMEADKVAQPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 240
DB 204 OLIDMEADKVAQPLRLSALPAGWFIADKSGAGERSGIIAALGPDGKPSRIVIYTTG 263
QY 241 SOATWDERNRQIAETGASLIKHW 263
DB 264 SOATWDERNRQIAETGASLIKHW 286

RESULT 11
US-09-490-070A-265
Sequence 265, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilaq, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAllister
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
DB 84 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAGPLLRSLPAGWFIADKSGAGRGSGIITAAIGPDGKPSRIIVITYTG 240
DB 204 QLIIMWEADKVAGPLLRSLPAGWFIADKSGAGRGSGIITAAIGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAEIGASLIRKM 263
DB 264 SOATMDERNRQIAEIGASLIRKM 286

RESULT 12
US-09-490-070A-362
Sequence 362, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAlliff
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQIGARVGYIELDINSKLTIESFRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKXDAEDQIGARVGYIELDINSKLTIESFRPERPPMSTFVLLCGAVLSRID 83

QY 61 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
DB 84 AGOELGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAGPLLRSLPAGWFIADKSGAGRGSGIITAAIGPDGKPSRIIVITYTG 240
DB 204 QLIIMWEADKVAGPLLRSLPAGWFIADKSGAGRGSGIITAAIGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAEIGASLIRKM 263
DB 264 SOATMDERNRQIAEIGASLIRKM 286

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOREPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQIGARVGYIELDINSKLTIESFRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKXDAEDQIGARVGYIELDINSKLTIESFRPERPPMSTFVLLCGAVLSRID 83

Db 24 HPEITLVKVDABDQAGARVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
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Db 84 AGQEBQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGRP 143
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Db 144 KELTAFLLNMGDHYTRLDRWPELNEAIPNDRDITPMVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
Db 204 QUIDMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
Db 264 SOATMDERNRQIAETGASLIRKM 286

RESULT 14

US-09-490-153-362
; Sequence 362, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Haag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQAGARVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 60

Db 24 HPEITLVKVDABDQAGARVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGRP 120
Db 84 AGQEBQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGRP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEAIPNDRDITPMVAAATTIRKLLTGELTLASRQ 180
Db 144 KELTAFLLNMGDHYTRLDRWPELNEAIPNDRDITPMVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
Db 204 QUIDMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
Db 264 SOATMDERNRQIAETGASLIRKM 286

RESULT 15

US-10-191-966-7
; Sequence 7, Application US/10191966
; Patent No. 6790612
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1348; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.2e-141;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDABDQAGARVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDABDQAGARVGYIELDLSGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEBQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGRP 120
Db 84 AGQEBQGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGRP 143
QY 121 KELTAFLLNMGDHYTRLDRWPELNEAIPNDRDITPMVAAATTIRKLLTGELTLASRQ 180
Db 144 KELTAFLLNMGDHYTRLDRWPELNEAIPNDRDITPMVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 240
Db 204 QUIDMWEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITYTG 263
QY 241 SOATMDERNRQIAETGASLIRKM 263
Db 264 SOATMDERNRQIAETGASLIRKM 286

Search completed: June 10, 2005, 11:01:13

Fri Jun 10 14:22:56 2005

us-10-668-778-2.rat

Page 8

Job time : 27.9646 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 15.2765 Seconds

(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149

Perfect score: 770
Sequence: 1 HPELVKVKADMDQAGARVG.....MGDHYTRDRKPEELNAIP 149

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	286	1	US-07-721-775A-2
2	770	100.0	286	1	US-08-339-658-2
3	770	100.0	286	3	US-09-263-933-7
4	770	100.0	286	3	US-09-263-933-14
5	770	100.0	286	3	US-09-263-933-21
6	770	100.0	286	3	US-09-025-769B-265
7	770	100.0	286	3	US-09-025-769B-362
8	770	100.0	286	4	US-09-919-901-7
9	770	100.0	286	4	US-09-919-901-14
10	770	100.0	286	4	US-09-919-901-21
11	770	100.0	286	4	US-09-490-070A-265
12	770	100.0	286	4	US-09-490-070A-362
13	770	100.0	286	4	US-09-490-153-265
14	770	100.0	286	4	US-09-490-153-362
15	770	100.0	286	4	US-10-191-966-7
16	770	100.0	286	4	US-10-191-966-14
17	770	100.0	286	4	US-10-191-966-21
18	770	100.0	286	4	US-09-490-324-265
19	770	100.0	286	4	US-09-490-324-362
20	770	100.0	286	4	US-09-025-769B-285
21	770	100.0	286	3	US-09-025-769B-298
22	770	100.0	286	3	US-09-025-769B-300
23	770	100.0	286	4	US-09-490-070A-285
24	770	100.0	286	4	US-09-490-070A-298
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27	770	100.0	286	4	US-09-490-153-298

28	770	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	770	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	770	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	770	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	770	100.0	299	3	US-09-263-933-2	Sequence 2, Appl1
33	770	100.0	299	3	US-09-263-933-9	Sequence 9, Appl1
34	770	100.0	299	3	US-09-263-933-16	Sequence 16, Appl1
35	770	100.0	299	3	US-09-919-901-2	Sequence 2, Appl1
36	770	100.0	299	4	US-09-919-901-9	Sequence 9, Appl1
37	770	100.0	299	4	US-09-919-901-16	Sequence 16, Appl1
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40	770	100.0	299	4	US-10-191-966-16	Sequence 16, Appl1
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42	769	99.9	265	2	US-08-719-697-2	Sequence 2, Appl1
43	769	99.9	265	3	US-08-727-616A-2	Sequence 2, Appl1
44	769	99.9	265	4	US-09-481-756-2	Sequence 2, Appl1
45	769	99.9	286	2	US-08-719-697-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-07-721-775A-2
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Relising, Ethnigton, Barnard, Perry & Milton
; STREET: P. O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07721,775A
; FILING DATE: 19910627
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-721-775A-2

Query Match 100.0%; Score 770; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.98-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADMDQAGARVGIEIDLNSGKILSFRRPFRPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKADMDQAGARVGIEIDLNSGKILSFRRPFRPMSTFVLLCGAVLSRID 83

Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
Qy 121 KETLAFILNMGDHVTRLDRMEPELNEAIP 149
Db 144 KETLAFILNMGDHVTRLDRMEPELNEAIP 172

RESULT 2

US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
NUMBER OF SEQUENCES: 2
MUTAGENICITY OF A CHEMICAL
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethlington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 770; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADQEDLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVKADQEDLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
Qy 121 KETLAFILNMGDHVTRLDRMEPELNEAIP 149
Db 144 KETLAFILNMGDHVTRLDRMEPELNEAIP 172

RESULT 3
US-09-263-933-7

Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1998-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADQEDLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVKADQEDLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143
Qy 121 KETLAFILNMGDHVTRLDRMEPELNEAIP 149
Db 144 KETLAFILNMGDHVTRLDRMEPELNEAIP 172

RESULT 4

US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADQEDLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVKADQEDLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
Qy 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
Db 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 143

QY 121 KETLAFHNMGDHVTRLDRWEPLENAIP 149
Db 144 KETLAFHNMGDHVTRLDRWEPLENAIP 172

RESULT 5
US-09-263-933-21
Sequence 21, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PR
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPELVVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83

QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGP 120
Db 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGP 143

QY 121 KETLAFHNMGDHVTRLDRWEPLENAIP 149
Db 144 KETLAFHNMGDHVTRLDRWEPLENAIP 172

RESULT 6
US-09-025-769B-265
Sequence 265, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vlc
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
Db 24 HPELVVVKQAEQDQGVGVGIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83

QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGP 120
Db 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGP 143

QY 121 KETLAFHNMGDHVTRLDRWEPLENAIP 149
Db 144 KETLAFHNMGDHVTRLDRWEPLENAIP 172

RESULT 7
US-09-025-769B-362
Sequence 362, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vlc
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090

;; INFORMATION FOR SEQ ID NO: 362:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULAR TYPE: protein
US-09-025-7698-362

Query Match 100.0%; Score 770; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 143
QY 121 KETLAFLLNMGDHVTSLDRWEPELNEAIP 149
DB 144 KETLAFLLNMGDHVTSLDRWEPELNEAIP 172

RESULT 8
US-09-919-901-7

;; Sequence 7, Application US/09919901
;; Patent No. 6599738
;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 7
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 143
QY 121 KETLAFLLNMGDHVTSLDRWEPELNEAIP 149
DB 144 KETLAFLLNMGDHVTSLDRWEPELNEAIP 172

RESULT 9
US-09-919-901-14
;; Sequence 14, Application US/09919901
;; Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 143
QY 121 KETLAFLLNMGDHVTSLDRWEPELNEAIP 149
DB 144 KETLAFLLNMGDHVTSLDRWEPELNEAIP 172

RESULT 10
US-09-919-901-21

;; Sequence 21, Application US/09919901
;; Patent No. 6599738
;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 60
DB 24 HPEVLVVKDAEDQLGARVGIETLDNSGKILSFRRPRPPMSTFKVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 120
DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATISMDTANLLTTIGGP 143
QY 121 KETLAFLLNMGDHVTSLDRWEPELNEAIP 149
DB 144 KETLAFLLNMGDHVTSLDRWEPELNEAIP 172

Db 24 HPEITLVKVDADDOUGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
 Db 84 AGQEQIGRRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTSFLLNMGDHVTRLDRWEPELNEAIP 149
 Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

RESULT 11

US-09-490-070A-265
 ; Sequence 265, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilaq, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
 ; White & McAuliffe
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,070A
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colin G. Sandercock, Esq.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 37629-0005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 912-2000
 ; TELEFAX: (202) 912-2020
 ; INFORMATION FOR SEQ ID NO: 265:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 286 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
 US-09-490-070A-265

Query Match 100.0%; Score 770; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.9e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOUGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 Db 24 HPEITLVKVDADDOUGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
 Db 84 AGQEQIGRRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTSFLLNMGDHVTRLDRWEPELNEAIP 149
 Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

RESULT 12

US-09-490-070A-362
 ; Sequence 362, Application US/09490070A
 ; Patent No. 6696248
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; Pack, Peter
 ; Ilaq, Vic
 ; Ge, Liming
 ; Moroney, Simon
 ; Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
 ; White & McAuliffe
 ; STREET: 1666 K Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/490,070A
 ; FILING DATE: 24-Jan-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Colin G. Sandercock, Esq.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 37629-0005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 912-2000
 ; TELEFAX: (202) 912-2020
 ; INFORMATION FOR SEQ ID NO: 362:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 286 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
 US-09-490-070A-362

Query Match 100.0%; Score 770; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.9e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOUGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
 Db 24 HPEITLVKVDADDOUGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 120
 Db 84 AGQEQIGRRIRIHSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTSFLLNMGDHVTRLDRWEPELNEAIP 149
 Db 144 KELTSFLLNMGDHVTRLDRWEPELNEAIP 172

RESULT 13

US-09-490-153-265
 ; Sequence 265, Application US/09490153
 ; Patent No. 6706484
 ; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265;
US-09-490-153-265
Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKDAEDQAGARVGYIEIDLNSGKILSFRRPRRPPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGARVGYIEIDLNSGKILSFRRPRRPPMSTFVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAITMSDNTAANLLTTIGSP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIP 172
RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362;
US-09-490-153-362
Query Match 100.0%; Score 770; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.9e-84;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKDAEDQAGARVGYIEIDLNSGKILSFRRPRRPPMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGARVGYIEIDLNSGKILSFRRPRRPPMSTFVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAITMSDNTAANLLTTIGSP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMYRELCSAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIP 149
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIP 172
RESULT 15
US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 7
 ; LENGTH: 286
 ; TYPE: prt
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: :
 US-10-191-966-7

Query Match 100.0%; Score 770; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.9e-84;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPETLVKVDADPDQGARVGYIELDLSGKILESFRPERFPMMSTFEKYLGGAVLSRID	60
Db	24	HPETLVKVDADPDQGARVGYIELDLSGKILESFRPERFPMMSTFEKYLGGAVLSRID	83
Qy	61	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP	120
Db	84	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP	143
Qy	121	KELTAFLNMGDPVTRLDRMEPELNEAIP	149
Db	144	KELTAFLNMGDPVTRLDRMEPELNEAIP	172

Search completed: June 10, 2005, 11:01:14
 Job time : 15.2765 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 / Search time 23.3762 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_228

Perfect score: 1170
Sequence: 1 HPELVKVKADBDQAGRVG.....KSGAGERSRGIIALGPDG 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1170	100.0	286	3	US-09-263-933-7
4	1170	100.0	286	3	US-09-263-933-14
5	1170	100.0	286	3	US-09-263-933-21
6	1170	100.0	286	3	US-09-025-769B-265
7	1170	100.0	286	3	US-09-025-769B-362
8	1170	100.0	286	4	US-09-919-901-7
9	1170	100.0	286	4	US-09-919-901-14
10	1170	100.0	286	4	US-09-919-901-21
11	1170	100.0	286	4	US-09-490-070A-265
12	1170	100.0	286	4	US-09-490-070A-362
13	1170	100.0	286	4	US-09-490-153-265
14	1170	100.0	286	4	US-09-490-153-362
15	1170	100.0	286	4	US-10-191-966-7
16	1170	100.0	286	4	US-10-191-966-14
17	1170	100.0	286	4	US-10-191-966-21
18	1170	100.0	286	4	US-09-490-324-265
19	1170	100.0	286	4	US-09-490-324-362
20	1170	100.0	286	3	US-09-025-769B-285
21	1170	100.0	286	3	US-09-025-769B-298
22	1170	100.0	286	3	US-09-025-769B-300
23	1170	100.0	286	4	US-09-490-070A-285
24	1170	100.0	286	4	US-09-490-070A-298
25	1170	100.0	286	4	US-09-490-070A-300
26	1170	100.0	286	4	US-09-490-153-285
27	1170	100.0	286	4	US-09-490-153-298

28	1170	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	1170	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	1170	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	1170	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	1170	100.0	299	3	US-09-263-933-2	Sequence 2, Appl
33	1170	100.0	299	3	US-09-263-933-9	Sequence 9, Appl
34	1170	100.0	299	3	US-09-263-933-16	Sequence 16, Appl
35	1170	100.0	299	4	US-09-919-901-2	Sequence 2, Appl
36	1170	100.0	299	4	US-09-919-901-16	Sequence 16, Appl
37	1170	100.0	299	4	US-10-191-966-2	Sequence 2, Appl
38	1170	100.0	299	4	US-10-191-966-9	Sequence 9, Appl
39	1170	100.0	299	4	US-10-191-966-16	Sequence 16, Appl
40	1170	100.0	299	4	US-09-555-510B-9	Sequence 9, Appl
41	1169	99.9	286	4	US-10-231-013-9	Sequence 9, Appl
42	1169	99.9	286	4	US-09-170-496D-292	Sequence 292, App
43	1169	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl
44	1169	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl
45	1165	99.6	263	1	US-08-407-544-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-07-721-775A-2

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:

APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

TITLE OR INVENTION: METHOD AND CELL LINE FOR TESTING

TITLE OR INVENTION: MUTAGENICITY OF A CHEMICAL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSER: Relating, Echington, Barnard, Perry & Milton

STREET: P. O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07721,775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-07-721-775A-2

Query Match 100.0%; Score 1170; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7E-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGRVGTYELDINSKTLIESFRPEERPPMNSTFYVLGAVLSRID 60
DB 24 HPELVKVKADBDQAGRVGTYELDINSKTLIESFRPEERPPMNSTFYVLGAVLSRID 83

QY 61 AGGOLGRRHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRMBEPLNEALPNDERDITMVAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRMBEPLNEALPNDERDITMVAATTLRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 2
US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482

GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond P.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Reising, Ethington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 1170; DB 1: Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRMBEPLNEALPNDERDITMVAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRMBEPLNEALPNDERDITMVAATTLRKLLTSELTLASRQ 203

QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 3
US-09-263-933-7
Sequence 7, Application US/09263933
Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 1170; DB 3: Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAEDQAGARVGYIEIDLNSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRHYSONDIVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGCP 143
QY 121 KETLAFILNMGDHVTRLDRMBEPLNEALPNDERDITMVAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRMBEPLNEALPNDERDITMVAATTLRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QLIDMMEADKVAGPLRLSALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 4
US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADQAGVGYIELDINSKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB HPELVKVKDADQAGVGYIELDINSKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHTRLDRWPELNEAIPNDRDPTMPVAAATTIRKLLTGELLTLASRQ 180
DB KELTAFILNMGDHTRLDRWPELNEAIPNDRDPTMPVAAATTIRKLLTGELLTLASRQ 203
QY 191 QUIDMEADKVAQPLLRSLALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QUIDMEADKVAQPLLRSLALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 5

US-09-263-933-21
Sequence 21, Application US/09263933
Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roderica L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 1170; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 6.7e-122;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADQAGVGYIELDINSKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB HPELVKVKDADQAGVGYIELDINSKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHTRLDRWPELNEAIPNDRDPTMPVAAATTIRKLLTGELLTLASRQ 180
DB KELTAFILNMGDHTRLDRWPELNEAIPNDRDPTMPVAAATTIRKLLTGELLTLASRQ 203
QY 191 QUIDMEADKVAQPLLRSLALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QUIDMEADKVAQPLLRSLALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 6

US-09-025-769B-265
Sequence 265, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 1170; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 6.7e-122;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADQAGVGYIELDINSKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
DB HPELVKVKDADQAGVGYIELDINSKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB AGOELGRRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHTRLDRWPELNEAIPNDRDPTMPVAAATTIRKLLTGELLTLASRQ 180
DB KELTAFILNMGDHTRLDRWPELNEAIPNDRDPTMPVAAATTIRKLLTGELLTLASRQ 203
QY 191 QUIDMEADKVAQPLLRSLALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QUIDMEADKVAQPLLRSLALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 7
US-09-025-769B-362
Sequence 362, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-362

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGRVGTYIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADQDQAGRVGTYIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYSDNTAANLLTTIGCP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHYTRLDRWEPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 203
QY 181 QLIWMEDKVAAGPLRLSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB 204 QLIWMEDKVAAGPLRLSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGRVGTYIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADQDQAGRVGTYIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYSDNTAANLLTTIGCP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHYTRLDRWEPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 203
QY 181 QLIWMEDKVAAGPLRLSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB 204 QLIWMEDKVAAGPLRLSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADQDQAGRVGTYIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADQDQAGRVGTYIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYSDNTAANLLTTIGCP 120
DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAIIYSDNTAANLLTTIGCP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHYTRLDRWEPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 203
QY 181 QLIWMEDKVAAGPLRLSALPAGWFIADKSGAGRGSRGIIAALGPDG 228

Db 204 QUIDMEADKVAAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 10
US-09-919-901-21
Sequence 21, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potce, Karen E.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-21

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKQKADBDQAGAVGYIELDINSKILIESFRPERPFPMSFTFKVLLCGAVLSRID 60
Db 24 HPEITLVKQKADBDQAGAVGYIELDINSKILIESFRPERPFPMSFTFKVLLCGAVLSRID 83

Qy 61 AGQEQGLGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
Db 84 AGQEQGLGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143

Qy 121 KELTFLNMGDHYTRLRWEPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 180
Db 144 KELTFLNMGDHYTRLRWEPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 203

Qy 181 QUIDMEADKVAAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QUIDMEADKVAAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 11
US-09-490-070A-265
Sequence 265, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAniff
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKQKADBDQAGAVGYIELDINSKILIESFRPERPFPMSFTFKVLLCGAVLSRID 60
Db 24 HPEITLVKQKADBDQAGAVGYIELDINSKILIESFRPERPFPMSFTFKVLLCGAVLSRID 83

Qy 61 AGQEQGLGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
Db 84 AGQEQGLGRIRHYSONDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143

Qy 121 KELTFLNMGDHYTRLRWEPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 180
Db 144 KELTFLNMGDHYTRLRWEPELNEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 203

Qy 181 QUIDMEADKVAAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QUIDMEADKVAAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 12
US-09-490-070A-362
Sequence 362, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAniff
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 1170; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 6,7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 144 KETLAFILNMGDHYTRLDRWEPPELNEAIPNDRDTTVPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB 204 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: KORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 1170; DB 4; Length 286;
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Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
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RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Poter, Karen B.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: :
US-10-191-966-7

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Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2005, 10:40:16 ; Search time 76.3841 Seconds
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Title: US-10-668-778-2_COPY_1_228

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	1170	100.0	286 10 US-09-919-901-7	Sequence 7, Appl1
3	1170	100.0	286 10 US-09-919-901-14	Sequence 14, Appl1
4	1170	100.0	286 10 US-09-919-901-21	Sequence 21, Appl1
5	1170	100.0	286 11 US-09-837-306-154	Sequence 34, Appl1
6	1170	100.0	286 14 US-10-191-966-7	Sequence 7, Appl1
7	1170	100.0	286 14 US-10-191-966-14	Sequence 14, Appl1
8	1170	100.0	286 14 US-10-191-966-21	Sequence 21, Appl1
9	1170	100.0	286 15 US-10-045-674-523	Sequence 523, Appl1
10	1170	100.0	286 16 US-10-416-708A-73	Sequence 73, Appl1
11	1170	100.0	2307 10 US-09-919-901-2	Sequence 2, Appl1

12	1170	100.0	2307 10 US-09-919-901-9	Sequence 9, Appl1
13	1170	100.0	2307 10 US-09-919-901-16	Sequence 16, Appl1
14	1170	100.0	2307 14 US-10-191-966-2	Sequence 2, Appl1
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16	1170	100.0	2307 14 US-10-191-966-16	Sequence 16, Appl1
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18	1169	99.9	286 14 US-10-842-534-9	Sequence 9, Appl1
19	1169	99.9	1293 14 US-10-251-385-292	Sequence 292, Appl1
20	1169	99.9	1967 16 US-10-477-044-1	Sequence 1, Appl1
21	1165	99.6	265 9 US-09-772-114-6	Sequence 6, Appl1
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23	1165	99.6	265 17 US-10-656-029-2	Sequence 2, Appl1
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30	1162	99.3	264 17 US-10-877-952-18	Sequence 18, Appl1
31	1162	99.3	362 15 US-10-469-199-2	Sequence 2, Appl1
32	1162	99.3	584 17 US-10-890-675-2	Sequence 2, Appl1
33	1158	99.0	265 9 US-09-772-114-8	Sequence 8, Appl1
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35	1158	99.0	265 16 US-10-622-088-114	Sequence 114, Appl1
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44	1121	95.8	284 15 US-10-052-188-2	Sequence 2, Appl1
45	470.5	40.2	288 14 US-10-016-668-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-668-778-2
Sequence 2, Application US/10668778
Publication No. US2004003817A1
GENERAL INFORMATION:
APPLICANT: Balint, Robert F.
APPLICANT: Her, Deng-Hong
APPLICANT: Kalobilos, Inc.
TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668, 778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526, 106
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135, 926
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175, 968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

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Best Local Similarity 100.0%; Pred. No. 8.1e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-7
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Best Local Similarity 100.0%; Pred. No. 9,2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

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US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
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; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
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Best Local Similarity 100.0%; Pred. No. 9,2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

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US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 286
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-21
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- Query Match 100.0%; Score 1170; DB 10; Length 286;
Best Local Similarity 100.0%; Pred. No. 9,2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 204 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGRIIAALGPDG 251

RESULT 5
US-09-837-306-354
; Sequence 354, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS
; FILE REFERENCE: DYAK/002
; CURRENT FILING DATE: 2001-09-24
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 354
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: pCCESS
US-09-837-306-354

Query Match 100.0%; Score 1170; DB 11; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGVGYIELDLSNGKILIESFRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGVGYIELDLSNGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVEELCSAATVMSDNTAANLLTTIGSP 120
Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVEELCSAATVMSDNTAANLLTTIGSP 143
Qy 121 KEITAFILNMGDHYTRLDRMEPELNEAIPNDRDITTMVAMATTIRKLLTSELTLASRQ 180
Db 144 KEITAFILNMGDHYTRLDRMEPELNEAIPNDRDITTMVAMATTIRKLLTSELTLASRQ 203
Qy 181 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGRIIAALGPDG 228
Db 204 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGRIIAALGPDG 251

RESULT 6
US-10-191-966-7
; Sequence 7, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1170; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGVGYIELDLSNGKILIESFRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGVGYIELDLSNGKILIESFRPERPMMSTFKVLLCGAVLSRID 83
Qy 61 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVEELCSAATVMSDNTAANLLTTIGSP 120
Db 84 AGQEQGRRIHYSQNDLVEYSPVTEKHLTDGWTVEELCSAATVMSDNTAANLLTTIGSP 143
Qy 121 KEITAFILNMGDHYTRLDRMEPELNEAIPNDRDITTMVAMATTIRKLLTSELTLASRQ 180
Db 144 KEITAFILNMGDHYTRLDRMEPELNEAIPNDRDITTMVAMATTIRKLLTSELTLASRQ 203
Qy 181 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGRIIAALGPDG 228
Db 204 QLIDMEADKVAAGPLRLSALPAGWFIADKSGAGERGSGRIIAALGPDG 251

RESULT 7
US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potes, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 2002-07-10
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-14

Query Match 100.0%; Score 1170; DB 14; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2e-113;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVDADQAGVGYIELDLSNGKILIESFRPERPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGVGYIELDLSNGKILIESFRPERPMMSTFKVLLCGAVLSRID 83

QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 120
 DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 143
 QY 121 KETLAFILNMGDHTRLDREWEPELNEALPNDERDTTPVMAATLRKLLTSELTLASRQ 180
 DB 144 KETLAFILNMGDHTRLDREWEPELNEALPNDERDTTPVMAATLRKLLTSELTLASRQ 203
 QY 181 QLIDMEADKVAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 228
 DB 204 QLIDMEADKVAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 251

RESULT 8
 US-10-191-966-21
 ; Sequence 21, Application US/10191966
 ; Publication No. US20030175692N1
 ; GENERAL INFORMATION:
 ; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patick, Amy K.
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT APPLICATION NUMBER: US/10/191,966
 ; CURRENT FILING DATE: 2002-07-10
 ; PRIOR APPLICATION NUMBER: US/09/263,933
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/129,611
 ; PRIOR FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: :
 US-10-191-966-21

Query Match 100.0%; Score 1170; DB 14; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.2e-113;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQAGVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKQADQDQAGVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 120
 DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 143
 QY 121 KETLAFILNMGDHTRLDREWEPELNEALPNDERDTTPVMAATLRKLLTSELTLASRQ 180
 DB 144 KETLAFILNMGDHTRLDREWEPELNEALPNDERDTTPVMAATLRKLLTSELTLASRQ 203
 QY 181 QLIDMEADKVAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 228
 DB 204 QLIDMEADKVAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 251

RESULT 9
 US-10-045-674-523
 ; Sequence 523, Application US/10045674
 ; Publication No. US2003023233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LADNER, ROBERT C.
 ; APPLICANT: COHEN, EDWARD H.
 ; APPLICANT: NASTRI, HORACIO G.
 ; APPLICANT: ROOKEY, KRISTIN L.
 ; APPLICANT: HOET, RENE
 ; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
 ; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
 ; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
 ; TITLE OF INVENTION: LIBRARIES
 ; FILE REFERENCE: DVA/002 CIP2
 ; CURRENT APPLICATION NUMBER: US/10/045,674
 ; CURRENT FILING DATE: 2001-10-25
 ; PRIOR APPLICATION NUMBER: 60/198,069
 ; PRIOR FILING DATE: 2000-04-17
 ; PRIOR APPLICATION NUMBER: 09/837,306
 ; PRIOR FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 635
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 523
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS
 ; OTHER INFORMATION: protein sequence
 US-10-045-674-523

Query Match 100.0%; Score 1170; DB 15; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.2e-113;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQAGVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKQADQDQAGVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 83
 QY 61 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 120
 DB 84 AGGOLGRRIHYSONDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGP 143
 QY 121 KETLAFILNMGDHTRLDREWEPELNEALPNDERDTTPVMAATLRKLLTSELTLASRQ 180
 DB 144 KETLAFILNMGDHTRLDREWEPELNEALPNDERDTTPVMAATLRKLLTSELTLASRQ 203
 QY 181 QLIDMEADKVAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 228
 DB 204 QLIDMEADKVAGPLRLSALPAGWFIADKSGAGERGSGIITIALGPDG 251

RESULT 10
 US-10-416-708A-73
 ; Sequence 73, Application US/10416708A
 ; Publication No. US20040161753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wise, John G.
 ; APPLICANT: Fromknecht, Katja
 ; TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
 ; TITLE OF INVENTION: SPECIFICITIES
 ; FILE REFERENCE: 37779-0004
 ; CURRENT APPLICATION NUMBER: US/10/416,708A
 ; CURRENT FILING DATE: 2004-01-28
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: Patent In version 3.2
 ; SEQ ID NO 73
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Construct
 US-10-416-708A-73

Query Match 100.0%; Score 1170; DB 16; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.2e-113;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQAGVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKQADQDQAGVGYIELDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 83

Qy 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
| | | | |
Db 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 143
| | | | |
Qy 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELLTLASRQ 180
| | | | |
Db 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELLTLASRQ 203
| | | | |
Qy 181 OLIDMMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 228
| | | | |
Db 204 OLIDMMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 251
| | | | |

RESULT 11

US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: :
US-09-919-901-2

Query Match 100.0%; Score 1170; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVKDABDQAGAVGYIELDINSKLTIESFRPERFPWMTFFVLLCGAVLSRID 60
| | | | |
Db 2045 HPEITLVKVKDABDQAGAVGYIELDINSKLTIESFRPERFPWMTFFVLLCGAVLSRID 2104
| | | | |
Qy 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
| | | | |
Db 2105 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 2164
| | | | |
Qy 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELLTLASRQ 180
| | | | |
Db 2165 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELLTLASRQ 2224
| | | | |
Qy 181 OLIDMMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 228
| | | | |
Db 2225 OLIDMMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 2272
| | | | |

RESULT 12

US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: :
US-09-919-901-9

Query Match 100.0%; Score 1170; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVKDABDQAGAVGYIELDINSKLTIESFRPERFPWMTFFVLLCGAVLSRID 60
| | | | |
Db 2045 HPEITLVKVKDABDQAGAVGYIELDINSKLTIESFRPERFPWMTFFVLLCGAVLSRID 2104
| | | | |
Qy 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
| | | | |
Db 2105 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 2164
| | | | |
Qy 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELLTLASRQ 180
| | | | |
Db 2165 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELLTLASRQ 2224
| | | | |
Qy 181 OLIDMMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 228
| | | | |
Db 2225 OLIDMMEADKVAAGPLRSALPAGWFIADKSGGERSGIIAALGPDG 2272
| | | | |

RESULT 13

US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: :
US-09-919-901-16

Query Match 100.0%; Score 1170; DB 10; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HPEITLVKVKDABDQAGAVGYIELDINSKLTIESFRPERFPWMTFFVLLCGAVLSRID 60
| | | | |
Db 2045 HPEITLVKVKDABDQAGAVGYIELDINSKLTIESFRPERFPWMTFFVLLCGAVLSRID 2104
| | | | |
Qy 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGCP 120
| | | | |

Db 2105 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFALHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
Db 2225 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 2272

RESULT 14
US-10-191-966-2
Sequence 2, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-2

Query Match 100.0%; Score 1170; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1,7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFALHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
Db 2225 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 2272

RESULT 15
US-10-191-966-9
Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-9

Query Match 100.0%; Score 1170; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 1,7e-111;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
Db 2045 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFRRPERPPMSTFVLLCGAVLSRID 2104
QY 61 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
Db 2105 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 2164
QY 121 KETAFALHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KETAFALHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 228
Db 2225 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGERGSRGIIAALGPDG 2272

Search completed: June 10, 2005, 11:09:07
Job time : 77.3841 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 63.6534 Seconds

(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975
Sequence: 1 HPELVKVKYKADBDQAGARVG.....GELITLASRQQLIDWMDK 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	975	100.0	229	2 O6WY5 Klebsiella
2	975	100.0	232	2 O6WY4 Klebsiella
3	975	100.0	241	2 O6WY8 Klebsiella
4	975	100.0	242	2 O6WY3 Klebsiella
5	975	100.0	285	2 O6KB67 Klebsiella
6	975	100.0	286	2 O38058 Klebsiella
7	975	100.0	286	2 O00626 Klebsiella
8	975	100.0	286	2 O79C16 Klebsiella
9	975	100.0	286	2 O79DR3 Klebsiella
10	970	99.5	225	2 O38212 Klebsiella
11	970	99.5	232	2 O6PRU7 Klebsiella
12	970	99.5	255	2 O84H50 Klebsiella
13	970	99.5	261	2 O84H49 Klebsiella
14	970	99.5	264	2 O6FRU6 Klebsiella
15	970	99.5	281	2 O6QIV0 Klebsiella
16	970	99.5	282	2 O6QIV1 Klebsiella
17	970	99.5	286	1 BLAT_ECOLI
18	970	99.5	286	1 BLAT_SALTI
19	970	99.5	286	2 O53043 Klebsiella
20	970	99.5	286	2 O8KSD3 Klebsiella
21	970	99.5	286	2 O8YF43 Klebsiella
22	970	99.5	286	2 O93328 Klebsiella
23	970	99.5	286	2 O934D7 Klebsiella
24	970	99.5	286	2 O934D7 Klebsiella
25	970	99.5	286	2 O934D7 Klebsiella
26	970	99.5	286	2 O934D7 Klebsiella
27	970	99.5	286	2 O6LBN9 Klebsiella
28	970	99.5	286	2 O6LBN9 Klebsiella
29	970	99.5	286	2 O6LBN9 Klebsiella
30	970	99.5	286	2 O6LBN9 Klebsiella
31	970	99.5	286	2 O6W7J4 Klebsiella

32	970	99.5	286	2 O6W9J1 Klebsiella
33	970	99.5	286	2 O6W9J2 Klebsiella
34	970	99.5	286	2 O6W9J3 Klebsiella
35	970	99.5	286	2 O7B3X5 Klebsiella
36	970	99.5	286	2 O7B899 Klebsiella
37	970	99.5	286	2 O7B899 Klebsiella
38	970	99.5	286	2 O7B899 Klebsiella
39	970	99.5	286	2 O7B899 Klebsiella
40	970	99.5	286	2 O7B899 Klebsiella
41	970	99.5	286	2 O7B899 Klebsiella
42	970	99.5	286	2 O7B899 Klebsiella
43	970	99.5	286	2 O7B899 Klebsiella
44	970	99.5	286	2 O7B899 Klebsiella
45	970	99.5	286	2 O7B899 Klebsiella

ALIGNMENTS

RESULT 1				
ID	O6WY5	PRELIMINARY;	PRT;	229 AA.
AC	O6WY5;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Beta-lactamase (Fragment).			
GN	Name=Blactem;			
OS	Klebsiella oxytoca.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Klebsiella.			
OX	NCBI_TaxID=571;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MISC126;			
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;			
RL	Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AY265885; AAP3843.1; -			
DR	HSP; P00807; IKGE.			
DR	InterPro; IPR000871; Beta_lactamase_A.			
DR	PRINTS; PR00118; BLACTAMASEA.			
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
FT	NON_TER 1 1			
FT	NON_TER 229 229			
SQ	SEQUENCE 229 AA; 25067 MW; C85582C2617F4467 CRC64;			
Query Match 100.0%; Score 975; DB 2; Length 229;				
Best Local Similarity 100.0%; Pred. No. 2.5e-74;				
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 HPELVKVKYKADBDQAGARVGITIEDLNSGKTIIESFRPEERPPMSTFKVLUCGAVLSRID 60			
DB	2 HPELVKVKYKADBDQAGARVGITIEDLNSGKTIIESFRPEERPPMSTFKVLUCGAVLSRID 61			
QY	61 AGQEQIGRIHYSDUDVYSPYTKHLTDGATVRELCSAITSNDTAAANLLTTIGCP 120			
DB	62 AGQEQIGRIHYSDUDVYSPYTKHLTDGATVRELCSAITSNDTAAANLLTTIGCP 121			
QY	121 KELTAFILNMGDHYTRLDWPEBELNEALPNDERDTTVPVAAATTKRLTGLTLTASRQ 180			
DB	122 KELTAFILNMGDHYTRLDWPEBELNEALPNDERDTTVPVAAATTKRLTGLTLTASRQ 181			
QY	181 QIIDWMDK 190			
DB	182 QIIDWMDK 191			
RESULT 2				
ID	O6WY4	PRELIMINARY;	PRT;	232 AA.
AC	O6WY4;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			

DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Hafnia alvei.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Hafnia.
 OX NCBI_TaxID=569;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC198;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265886; AAP3844.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 232
 FT SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;
 SQ

Query Match 100.0%; Score 975; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 2.5e-74;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMSTFVLLCGAVLSRID 60
 DB 2 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMSTFVLLCGAVLSRID 61
 QY 61 AGQEQGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 62 AGQEQGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 121
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 180
 DB 122 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 181
 QY 181 QLIDMMEADK 190
 DB 182 QLIDMMEADK 191

RESULT 3

Q6MWY8 PRELIMINARY; PRT; 241 AA.
 AC Q6MWY8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC112;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265882; AAP3840.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR00146; Beta_lactamase.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 241
 FT SEQUENCE 241 AA; 26407 MW; 38DF2AFD0C5807D CRC64;

Query Match 100.0%; Score 975; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.6e-74;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMSTFVLLCGAVLSRID 60
 DB 7 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMSTFVLLCGAVLSRID 66
 QY 61 AGQEQGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 67 AGQEQGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 126
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 180
 DB 127 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 186
 QY 181 QLIDMMEADK 190
 DB 187 QLIDMMEADK 196

RESULT 4

Q6MWY3 PRELIMINARY; PRT; 242 AA.
 AC Q6MWY3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP3845.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR000871; Beta_lactamase.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 242
 FT SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 975; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 2.6e-74;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMSTFVLLCGAVLSRID 60
 DB 8 HPELVKVKADBDQAGAVGYIELDINSKILSFRRPFRPMSTFVLLCGAVLSRID 67
 QY 61 AGQEQGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 120
 DB 68 AGQEQGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGCP 127
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 180
 DB 128 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTTPVAAATTLRKLLTGBLLTLASRQ 187
 QY 181 QLIDMMEADK 190
 DB 188 QLIDMMEADK 197

RESULT 5

Q6KB67 PRELIMINARY; PRT; 285 AA.
 AC Q6KB67;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY265887; AAP3845.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR000871; Beta_lactamase.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 285
 FT SEQUENCE 285 AA; 30000 MW; 38C3DFA8A5A3807D CRC64;

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DR 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DB Hypothetical protein (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=First leaf;
RA Jansen C., Korell M., Ecker C., Biedenkopf D., Kogel K.H.;
RL Submitted (May-2004) to the EMBL/GenBank/DDJ databases.
DR EMBL; AJ717739; CAG30723.1; -.
DR HSSP; P00807; 1A0.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hypothetical protein.
FT NON_TER 285
SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.2e-74;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 60
DB HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 84 AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
DB 84 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 180
QY 121 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 180
DB 144 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 6
Q38058 PRELIMINARY; PRT; 286 AA.
ID Q38058;
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta lactamase.
GN Name=bla;
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirinae.
OX NCBI_TaxId=10847;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
RA Henrich B., Schmidberger B.;
RL "A variant of phiX174 gene B-based positive selection vectors with
enhanced lytic potential.";
RL Gene 154:51-54(1995).
RL EMBL; Z35638; CAA84692.1; -.
DR PIR; S47061; S47061.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.

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SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.2e-74;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 60
DB HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
QY 24 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
DB 24 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 84 AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
DB 84 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 180
QY 121 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 180
DB 144 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 7
Q00626 PRELIMINARY; PRT; 286 AA.
ID Q00626;
AC Q00626; O08022; O08102; O09393; O09396; O09397; O09398; O09399;
AC O09400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
AC O09408; O09481; O09482; O09483; O09490; Q57339;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Beta-lactamase.
OS Staphylococcus aureus.
OC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RC MEDLINE=9642275; PubMed=8825372; DOI=10.1006/plas.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RT "The staphylococcal insertion sequence IS257 is active.";
RL Plasmid 34:198-205(1995).
DR EMBL; U36912; AAB39957.1; -.
DR EMBL; U36911; AAB39956.1; -.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.2e-74;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 60
DB HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
QY 24 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
DB 24 HPELVKVKYADQAGARVGYIELDLSGKILSFSPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 84 AGQEQLGRRIRHSQNDLVEYSPTVEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
DB 84 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 180
QY 121 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 180
DB 144 KETLAFILNMGDHYVRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGLLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

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OS Bacteriophage f1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10863;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Radie J.S., Conrad M.;
RT "O-6-methylguanine mutation and repair is nonuniform: Selection for
DNA most interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885(1986).
DR EMBL; M14017; AAA32208.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 225;
Best Local Similarity 98.9%; Pred. No. 6,4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLGCAYLSRID 60
DB 24 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLGCAYLSRID 83
OY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120
DB 84 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 143
OY 121 KELITAFINMGDGHVRLDRWPELNEAIPNDRDTPMPAATTIRKLTGELTLASRQ 180
DB 144 KELITAFINMGDGHVRLDRWPELNEAIPNDRDTPMPAATTIRKLTGELTLASRQ 203
OY 181 OLIDWMEADK 190
DB 204 OLIDWMEADK 213

RESULT 11

OC PRU7 PRELIMINARY; PRT; 232 AA.

AC O6PRU7
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-U33;
RA Ghandali S., Hosseini-Mazini S.M.;
RL Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583761; AAS86427.1; -.
DR HSSP; P00807; 1ALO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285EE70BB0 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 232;
Best Local Similarity 98.9%; Pred. No. 6,4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLGCAYLSRID 60
DB 15 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLGCAYLSRID 74
OY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120
DB 75 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 134
OY 121 KELITAFINMGDGHVRLDRWPELNEAIPNDRDTPMPAATTIRKLTGELTLASRQ 180
DB 135 KELITAFINMGDGHVRLDRWPELNEAIPNDRDTPMPAATTIRKLTGELTLASRQ 194
OY 181 OLIDWMEADK 190
DB 195 OLIDWMEADK 204

RESULT 12

OC PRU7 PRELIMINARY; PRT; 255 AA.

AC O84H50
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanhal M.A.;
RL Submitted (Jun-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130282; AA05026.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 255;
Best Local Similarity 98.9%; Pred. No. 7,4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLGCAYLSRID 60
DB 12 HPEITVKKVADBDQAGRVGYIELDLSGKILSFPRPERFPMSTFKYLGCAYLSRID 71
OY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120
DB 72 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 131
OY 121 KELITAFINMGDGHVRLDRWPELNEAIPNDRDTPMPAATTIRKLTGELTLASRQ 180
DB 132 KELITAFINMGDGHVRLDRWPELNEAIPNDRDTPMPAATTIRKLTGELTLASRQ 191
OY 181 OLIDWMEADK 190
DB 192 OLIDWMEADK 201

RESULT 13

OC PRU7 PRELIMINARY; PRT; 261 AA.

AC O84H49
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).

OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanhal M.A., Verhoef J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
SQ SEQUENCE 261 AA; 28738 MW; 4F748F733A08CB8 CRC64;

Query Match 99.5%; Score 970; DB 2; Length 261;
Best Local Similarity 98.9%; Pred. No. 7.7e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRD 60
DB 12 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRD 71
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANILLTTIGSP 120
DB 72 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANILLTTIGSP 131
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 180
DB 132 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 191
QY 181 QLIDMWEADK 190
DB 192 QLIDMWEADK 201

RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
ID Q6PRU6;
AC Q6PRU6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=U11;
RA Ghandili S., Hoseini-Maziani S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583762; AAS86428.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
SQ SEQUENCE 264 AA; 28986 MW; A4F071CF7489352C CRC64;

Query Match 99.5%; Score 970; DB 2; Length 264;
Best Local Similarity 98.9%; Pred. No. 7.8e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRD 60

DB 12 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRD 71
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANILLTTIGSP 120
DB 72 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANILLTTIGSP 131
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 180
DB 132 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 191
QY 181 QLIDMWEADK 190
DB 192 QLIDMWEADK 201

RESULT 15
Q6QIV0 PRELIMINARY; PRT; 281 AA.
ID Q6QIV0;
AC Q6QIV0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (Fragment).
GN Name=BlatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yacubyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR000871; Beta_lactamase.
DR InterPro; IPR001466; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 281
SQ SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;

Query Match 99.5%; Score 970; DB 2; Length 281;
Best Local Similarity 98.9%; Pred. No. 8.4e-74;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRD 60
DB 24 HPEITLVKVKADBDQAGARVGYIELDLSGKILIESFRPERPMMSTPFVLLCGAVLSRD 83
QY 61 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQOLGRRIHYSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANILLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITPMVAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMWEADK 190
DB 204 QLIDMWEADK 213

Search completed: June 10, 2005, 10:57:02
Job time : 63.6534 secs

XX (PANO-) PANORAMA RES INC.

XX Balint RF, Her J;

XX WPI; 2001-451857/48.

DR N-PSDB; AAD10411.

PT Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.

PS Claim 36; Fig 2; 104pp; English.

XX The invention relates to new interaction-dependent enzyme association
CC (IdA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The IdA systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is Escherichia coli
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu

XX Sequence 263 AA;

Query Match 100.0%; Score 885; DB 4; Length 263;

Best Local Similarity 100.0%; Pred. No. 5.2e-90;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXADADQIGARVGYEIDNSGKILSPRPFRPMSTFKYLGGAVLSRD 60
DB 1 HPEITLVKXADADQIGARVGYEIDNSGKILSPRPFRPMSTFKYLGGAVLSRD 60
QY 61 AGOEOLGRIRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
DB 61 AGOEOLGRIRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
QY 121 KELTAFILHMGDVTRLDRWPEELNEAIPNDRDPTTVPVAMATTIRKLITGE 172
DB 121 KELTAFILHMGDVTRLDRWPEELNEAIPNDRDPTTVPVAMATTIRKLITGE 172

RESULT 2
AAB36692
ID AAB36692 standard; protein; 263 AA.
XX

AC AAB36692;
XX
XX 15-MAR-2001 (first entry)

DE Escherichia coli mature TEM-1 beta-lactamase protein sequence.

KW Interaction-activated protein; beta-lactamase; protein interaction.

XX Escherichia coli.

FN WO200071702-A1.

XX 30-NOV-2000.

XX 16-MAR-2000; 2000MO-US007108.

XX 25-MAY-1999; 99US-0135926P.

XX 13-JAN-2000; 2000US-0175968P.

XX (PANO-) PANORAMA RES INC.

PI Balint RF, Her J;

XX WPI; 2001-032034/04.

DR N-PSDB; AAC90773.

PT Novel fragment complementation system to identify interactions between
PT polypeptides comprises fragment pairs having first and second members
PT that reassemble into a marker protein which has a directly detectable
PT signal.

PS Disclosure; Fig 2; 94pp; English.

XX The present invention describes a fragment complementation system (I)
CC which comprises a first oligopeptide (OP1) containing an N-terminal
CC fragment with a C-terminal break point and a second oligopeptide (OP2)
CC comprising a C-terminal with a N-terminal breakpoint, in which the C and
CC N terminal fragments are both derived from a marker protein (MP) and
CC reassemble to form a functionally reconstituted MP. Methods from the
CC present invention are used for monitoring the occurrence of protein-
CC protein interactions in a sample, identifying epitopes that bind to an
CC between two different proteomes, identifying interactions between
CC immunoglobulin (Ig) variable region, for identifying interactions between
CC an extracellular domain of a transmembrane protein and a polypeptide, for
CC high-throughput identification of compounds that inhibit phosphorylation-
CC regulated signal transducers, forming a enzyme complementation system for
CC selecting simultaneous incorporation of multiple genetic elements into a
CC host cell and for activating a beta-lactam derivative of an antitumor
CC compound in a host who is in need of it. The present sequence represents
CC the Escherichia coli mature TEM-1 beta-lactamase, which is used in the
CC exemplification of the present invention

XX Sequence 263 AA;

Query Match 100.0%; Score 885; DB 4; Length 263;

Best Local Similarity 100.0%; Pred. No. 5.2e-90;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXADADQIGARVGYEIDNSGKILSPRPFRPMSTFKYLGGAVLSRD 60
DB 1 HPEITLVKXADADQIGARVGYEIDNSGKILSPRPFRPMSTFKYLGGAVLSRD 60
QY 61 AGOEOLGRIRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
DB 61 AGOEOLGRIRIHYSQNDLVEYSPTVEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
QY 121 KELTAFILHMGDVTRLDRWPEELNEAIPNDRDPTTVPVAMATTIRKLITGE 172
DB 121 KELTAFILHMGDVTRLDRWPEELNEAIPNDRDPTTVPVAMATTIRKLITGE 172

RESULT 3
AD67709

ID ADJ67709 standard; protein; 263 AA.
 XX ADJ67709;
 XX 20-MAY-2004 (first entry)
 XX Escherichia coli TEM-1 beta-lactamase.
 DE
 XX
 KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX
 OS Escherichia coli.
 XX
 PN US2004038317-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 22-SEP-2003; 2003US-00668778.
 XX
 PR 15-MAR-1999; 99US-0124339P.
 XX
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175688P.
 PR 15-MAR-2000; 2000US-00526106.
 XX
 PA (KALO-) KALOBIOS INC.
 XX
 PI Balint RF, Her J;
 XX
 DR WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47pp; English.
 XX
 CC The invention describes a fragment complementation system (I) comprising
 CC a first oligopeptide having an N-terminal fragment with a C-terminal
 CC break-point, and a second oligopeptide having a C-terminal fragment with
 CC a N-terminal break-point, where the N-terminal fragment and the C-
 CC terminal fragment each are derived from a marker protein and reassemble
 CC to form a functionally reconstituted marker protein. (I) is useful for
 CC selecting simultaneous incorporation of multiple genetic elements into a
 CC host cell, and activating a beta-lactam derivative of an anti-tumour
 CC compound in a host. The method described is useful for identifying a
 CC second oligopeptide to which a first oligopeptide binds, involving co-
 CC expressing the first and second oligopeptides. Binding of the first
 CC oligopeptide to the second oligopeptide results in the functional
 CC reassembly of the marker protein. The method is also useful for
 CC monitoring the occurrence of protein-protein interactions in a sample;
 CC identifying oligopeptide interactions between two different proteomes;
 CC and identifying epitopes that bind to an immunoglobulin variable region.
 CC (I) or an expression cassette (II), encoding a selectable N or C-terminal
 CC peptide, is useful for identifying interactions between an extra cellular
 CC domain of a transmembrane protein and a polypeptide, where the
 CC transmembrane protein is an immune cell protein, preferably CD40. (I) or
 CC (II) is useful for high-throughput identification of compound that
 CC inhibit phosphorylation-regulated cell signal transducers. (I)
 CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 CC
 CC Sequence 263 AA;
 XX
 XX

Query Match 100.0%; Score 885; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 5.2e-90;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HPETLVKVDADPDQARVGYIELDLSGKILESFRPFRPMPSTFKYLGCVALSRID 60
 DB 1 HETTLVKVDADPDQARVGYIELDLSGKILESFRPFRPMPSTFKYLGCVALSRID 60
 OY 61 AGGEOIGRRIRHVSQNDLVESPYTEKHLTDGKTTRELCSAATMSDNTAANLLTTIGCP 120
 DB 61 AGGEOIGRRIRHVSQNDLVESPYTEKHLTDGKTTRELCSAATMSDNTAANLLTTIGCP 120
 OY 121 KSLTAFIHMGGHVRIDRWEPELINAIPNDRSDTTMPVAMATTLLKLTGE 172
 DB 121 KSLTAFIHMGGHVRIDRWEPELINAIPNDRSDTTMPVAMATTLLKLTGE 172
 RESULT 4
 ID AAM16634
 XX AAM16634 standard; protein; 264 AA.
 AC AAM16634;
 XX
 DT 09-AUG-1997 (first entry)
 XX
 DE Beta-lactamase (including signal peptide).
 XX
 KM Gene directed enzyme prodnrg therapy; GDEPT;
 KM virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 XX
 OS Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Sig_peptide
 XX
 PN MO919180-A2.
 XX
 PD 29-MAY-1997.
 XX
 PF 19-NOV-1996; 96WO-GB002845.
 XX
 PR 20-NOV-1995; 95GB-00023703.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dev I, Moore JT, Ohmstede C;
 XX
 DR WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.
 XX
 PT Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 XX
 PS Example; Page 28; 38pp; English.
 XX
 CC Escherichia coli beta-lactamase (AAM16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnrg therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodnrg into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill
 XX
 XX Sequence 264 AA;
 XX
 XX
 Query Match 100.0%; Score 885; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 5.2e-90;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPPMSTFKYLTCGAVLSRID 60
DB      2 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPERPPMSTFKYLTCGAVLSRID 61
QY      61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 120
DB      62 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGCP 121
QY      121 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 172
DB      122 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 173

RESULT 5
AAW18680
ID      AAW18680 standard; protein; 264 AA.
XX      AC
XX      AAW18680;
XX      DT
XX      13-AUG-1997 (first entry)
XX      DE
XX      Intracellularly-expressed beta-lactamase.
XX      KW
XX      Producing therapy; gene directed enzyme producing therapy; GDBPT;
XX      virus directed enzyme producing therapy; VDEPT; lung cancer;
XX      beta-lactamase; PCMV-delBL.
XX      OS
XX      Escherichia coli.
XX      PN
XX      WO9719183-A2.
XX      PD
XX      29-MAY-1997.
XX      PF
XX      19-NOV-1996; 96WO-GB002846.
XX      PR
XX      20-NOV-1995; 95GB-00023703.
XX      PA
XX      (GLAXO) GLAXO GROUP LTD.
XX      PI
XX      Dev I, Moore JT, Sethna PB;
XX      WPI; 1997-298118/27.
XX      DR
XX      N-PSDB; AAT70311.
XX      PT
XX      DNA construct for gene-directed enzyme producing therapy of lung cancer -
XX      comprises lung- or neuroendocrine-specific promoter controlling
XX      expression of producing-converting enzyme.
XX      PS
XX      Example 811; Page 32-34; 53pp; English.
XX      CC
XX      The intracellular form (AAW18680) of TEM beta-lactamase is expressed by
XX      PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
XX      sequence, minus the signal sequence, is placed under control of the
XX      immediate/early promoter of cytomegalovirus. Intracellular beta-
XX      lactamase constructs, placed under control of promoter/enhancer elements
XX      of lung-associated protein or neuroendocrine marker protein genes, can be
XX      used in novel chimaeric molecules for use in producing therapy of lung
XX      cancer
XX      SQ
XX      Sequence 264 AA;

Query Match      100.0%; Score 885; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 5.2e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      121 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 172
DB      122 KELTAFILNMGDHTRLDRWEPELNEAIPNDRDRTTVPVAAATTIRKLLTGE 173

RESULT 6
AAR31575
ID      AAR31575 standard; protein; 286 AA.
XX      AC
XX      AAR31575;
XX      DT
XX      10-MAR-2003 (revised)
XX      04-JUN-1993 (first entry)
XX      DE
XX      Ampicillin resistance protein.
XX      KW
XX      CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;
XX      xenobiotics; circular; chimeric cytochrome P450IA1.
XX      OS
XX      Homo sapiens.
XX      PN
XX      US5180666-A.
XX      PD
XX      19-JAN-1993.
XX      PF
XX      27-JUN-1991; 91US-00721775.
XX      PR
XX      27-JUN-1991; 91US-00721775.
XX      PA
XX      (UYWA-) UNIV WAYNE STATE.
XX      PI
XX      States JC, Hines RN, Novak RF;
XX      WPI; 1993-052845/06.
XX      DR
XX      N-PSDB; AAQ36498.
XX      PT
XX      In vitro method for testing mutagenicity of a chemical - by metabolising
XX      chemical cell line consisting of transformed fibroblasts having
XX      detectable cytochrome P450 mixed function oxidase activity and detecting
XX      gene damage.
XX      PS
XX      Disclosure; Col 21-24; 24pp; English.
XX      CC
XX      The expression constructs PRNH127 and PRNH155 contain identical sequences
XX      but were constructed using different strategies (see AAQ36498). The
XX      constructs comprise exons 2-7 of human CYP1A1 gene under the control of
XX      the inducible mouse metallothionein (MMT-1) promoter. The constructs also
XX      contain an open reading frame in the opposite orientation to the
XX      cytochrome P450 exons. This ORF encodes ampicillin resistance. The
XX      constructs are suitable for transformation of human fibroblasts derived
XX      from the xeroderma pigmentosum group A. Cultures of the transformed
XX      fibroblasts can be used to test substances for mutagenicity. The presence
XX      of the inducible cytochrome P450 gene allows metabolism of the substance
XX      to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
XX      field.)
XX      SQ
XX      Sequence 286 AA;

Query Match      100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 144 KeltaFLNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTLRKLLTGE 195

RESULT 7

AA97619 standard; protein; 286 AA.

AA97619;

20-AUG-1996 (first entry)

Secretory beta-lactamase.

Gene therapy; gene directed enzyme prodnug therapy; GDEPT; virus directed enzyme prodnug therapy; VDBPT; prodnug activation; cytotoxic; cycostatic; cancer; tumour; retrovirus; vector; beta-lactamase; cephalosporin.

Synthetic.

WO9616179-A1.

30-MAY-1996.

20-NOV-1995; 95WO-GB002716.

18-NOV-1994; 94GB-00023367.

(WELL) WELLCOME FOUND LTD.

Dev IK, Moore JT, Ohmsted C;

WPI; 1996-268615/27.

N-PSDB; AAT29220.

Molecular chimaera for use in enzyme gene therapy - is activated in a target cell to express a secretable enzyme which cleaves a prodnug outside the cell into a cytotoxic or cycostatic agent.

Example 3; Page 57-58; 73pp; English.

A secretory beta-lactamase (AA97619) is expressed from DNA construct PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under the control of the intermediate/early cytomegalovirus promoter. Beta-lactamase delivery to mammalian cells confers sensitivity to cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours was increased upon i.t. injection of the secretory beta-lactamase DNA construct

Sequence 286 AA;

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPEITLVKVKADADQGAARVGYIELDLSGKILIESFRPERFPWSTFKYLLCGAVLSRID 60
24 HPEITLVKVKADADQGAARVGYIELDLSGKILIESFRPERFPWSTFKYLLCGAVLSRID 83
61 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 120
84 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 143
121 KeltaFLNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTLRKLLTGE 172
144 KeltaFLNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTLRKLLTGE 195

RESULT 8
AA96423 standard; protein; 286 AA.

XX AA96423;

AC 25-MAR-2003 (revised)
DT 25-NOV-1996 (first entry)

Cytochrome P450 (CYP1A1 construct).

cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay; metabolism.

Homo sapiens.

US5525482-A.

11-JUN-1996.

15-NOV-1994; 94US-00339658.

27-JUN-1991; 91US-00721775.

09-DEC-1992; 92US-00980295.

(UYMA-) UNIT WAYNE STATE.

Hines RN, Novak RF, States JC;

WPI; 1996-2686397/29.

N-PSDB; AAT30354.

Testing chemicals for cytotoxicity to human by detecting gene damage - using recombinant fibroblasts transformed with cytochrome P450 gene under control of inducible promoter.

Disclosure; Col 17-24; 26pp; English.

The present sequence is encoded by a chimeric mouse metallothionein-CYP1A1 construct. Two clones, PRNH127 and PRNH15, were isolated by different methods and which both had the same sequence. The CYP1A1 construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially toxic chemicals. The cells having been transformed to express cytochrome P450, under the control of a controllable promoter through the CYP1A1 gene, upon exposure to the chemical in vitro. The chemical is metabolised intracellularly into a cytochrome metabolite by oxidation within the fibroblasts through the intracellular cytochrome P450 mixed function oxidase enzymes expressed by the cells. Gene damage in the test cells is detected as an indication of cytotoxicity of the chemical. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 286 AA;

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HPEITLVKVKADADQGAARVGYIELDLSGKILIESFRPERFPWSTFKYLLCGAVLSRID 60
24 HPEITLVKVKADADQGAARVGYIELDLSGKILIESFRPERFPWSTFKYLLCGAVLSRID 83
61 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 120
84 AGQEBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAAANLLTTIGGP 143
121 KeltaFLNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTLRKLLTGE 172
144 KeltaFLNMGDHVTRLDRWBEPELNEAIPNDRDRTTTPVAAATTLRKLLTGE 195

RESULT 9
AAW16635 standard; protein; 286 AA.

```

AC AAW16635;
XX
XX 09-AUG-1997 (first entry)
XX
DE Beta-lactamase (no signal peptide).
XX
XX Gene directed enzyme prodng therapy; GDEPT;
XX virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;
XX HIV; inflammation.
XX
OS Escherichia coli.
XX
XX MO9719180-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002845.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Ohmsted C;
XX
XX MPI; 1997-298117/27.
XX
XX N-PSDB; AAT66737.
XX
XX Molecular chimera for gene or virus directed enzyme prodng therapy -
XX useful for treatment of cancer, viral infection or inflammation.
XX
XX Example; Page 26; 38pp; English.
XX
XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
XX is the expression product of a molecular chimera, designated PCMV-delBL
XX (AAT66738), in which the beta-lactamase gene is under control of the CMV
XX intermediate/early promoter. Vectors consisting of a transcriptional
XX regulatory DNA sequence linked to a beta-lactamase gene can be used for
XX enzyme prodng therapy. Intracellular expression of the beta-lactamase in
XX a targeted cell allows conversion of a prodng into an agent toxic to
XX the cell for treatment of cancer, viral (e.g. HIV) infection or
XX inflammation
XX
XX Sequence 286 AA;
XX
XX SQ
XX
Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKDAEDDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKDAEDDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGOQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGE 172
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGE 195

```

RESULT 10
AAW18679
ID AAW18679 standard; protein; 286 AA.

AC AAW18679;
XX
XX 13-AUG-1997 (first entry)
XX
XX Secretory beta-lactamase.
XX
XX Prodng therapy; gene directed enzyme prodng therapy; GDEPT;
XX virus directed enzyme prodng therapy; VDEPT; lung cancer;
XX

```

KW beta-lactamase; PCMV-BL.
XX
XX Escherichia coli.
XX
XX Key location/Qualifiers
XX Peptide 1..23
XX Protein /label= Sig_peptide
XX /label= 24..286
XX /label= Mat_protein
XX
XX MO9719183-A2.
XX
XX 29-MAY-1997.
XX
XX 19-NOV-1996; 96WO-GB002846.
XX
XX 20-NOV-1995; 95GB-00023703.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dev I, Moore JT, Sethna PB;
XX
XX MPI; 1997-298118/27.
XX
XX N-PSDB; AAT70309.
XX
XX DNA construct for gene-directed enzyme prodng therapy of lung cancer -
XX comprises lung- or neuroendocrine-specific promoter controlling
XX expression of prodng-converting enzyme.
XX
XX Example 81; Page 26-27; 53pp; English.
XX
XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by PCMV-
XX BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
XX placed under control of the intermediate/early promoter of
XX cytomegalovirus. Secretory beta-lactamase constructs, placed under
XX control of promoter/enhancer elements of lung- associated protein or
XX neuroendocrine marker protein genes, can be used in novel chimeric
XX molecules for use in prodng therapy of lung cancer
XX
XX Sequence 286 AA;
XX
XX SQ
XX
Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKDAEDDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKDAEDDQAGARVGYIEIDLNSGKILSFRRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGOQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGOQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGE 172
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIPNDRDITMVAATTLRKLLTGE 195

```

RESULT 11
AAI08529
ID AAI08529 standard; protein; 286 AA.

AC AAI08529;
XX
XX 03-AUG-1999 (first entry)
XX
XX Vector pASK75 beta-la protein.
XX
XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
XX tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
XX insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
XX allergy.
XX

OS Synthetic.
XX
XX MO9925866-A1.
XX
XX 27-MAY-1999.
XX
XX 11-NOV-1998; 98MO-FI000873.
XX
XX 14-NOV-1997; 97FI-00004235.
XX
XX (KORP/) KORBELA M.
XX (KARP/) KARP M.
XX (KURI/) KURITU J.
XX
XX Korpela M, Karp M, Kuritu J;
XX
XX WPI; 1999-338015/28.
XX N-PSDB; AAV72418.
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
XX
XX
XX Disclosure; Page 47-48; 67pp; English.
XX
XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline from other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxDABE
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (Tetr)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (Tetr) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,
CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected
XX
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITVKKDAEDDQAGAVGYIELDLSGKILSFRRPFRPMSFPVLLCGAVLSRID 60
DB 24 HPEITVKKDAEDDQAGAVGYIELDLSGKILSFRRPFRPMSFPVLLCGAVLSRID 83
QY 61 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KETLAFILNMGDHTRLDRWPELNEAIPNDRDRTTVPVAAATTIRKLLTGS 172
DB 144 KETLAFILNMGDHTRLDRWPELNEAIPNDRDRTTVPVAAATTIRKLLTGS 195
RESULT 12
AAB10442
ID AAB10442 standard; protein; 286 AA.
XX
XX AAB10442;
XX
XX 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX15G2 bla protein.
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX
XX OS Synthetic.
XX
XX DE19900635-A1.
XX
XX 13-JUL-2000.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX 11-JAN-1999; 99DE-01000635.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Breitling F, Poustka A, Moldenhauer G;
XX
XX WPI; 2000-499632/45.
XX N-PSDB; AAA71430.
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
XX
XX
XX Claim 16; Fig 3; 22pp; German.
XX
XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig; and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX15G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
XX
XX
SQ Sequence 286 AA;
Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITVKKDAEDDQAGAVGYIELDLSGKILSFRRPFRPMSFPVLLCGAVLSRID 60
DB 24 HPEITVKKDAEDDQAGAVGYIELDLSGKILSFRRPFRPMSFPVLLCGAVLSRID 83
QY 61 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOELGRIRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KETLAFILNMGDHTRLDRWPELNEAIPNDRDRTTVPVAAATTIRKLLTGS 172
DB 144 KETLAFILNMGDHTRLDRWPELNEAIPNDRDRTTVPVAAATTIRKLLTGS 195
RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.
XX
XX AAB10438;
XX
XX 01-DEC-2000 (first entry)
XX
XX Expression vector pSEX11L4 bla protein.
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW

XX bla resistance marker; recombinant host cell; saccharification;
KM fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KM glucanase; integration vector; pLO12306.
XX
OS unidentified.
XX
PN WO200071729-A2.
XX
PD 30-NOV-2000.
XX
PF 26-MAY-2000; 2000WO-US014773.
XX
PR 26-MAY-1999; 99US-0136376P.
XX (UYFL) UNIV FLORIDA RES FOUND.
XX
PI Ingram LO, Zhou S;
XX
XX
DR WPI: 2001-032043/04.
DR N-P5DB; AAC91455.
XX
XX
PT Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.
XX
XX
PS Disclosure; Page 82-83; 87pp; English.
XX
XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence
XX
SQ Sequence 286 AA;
XX
XX
Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-90;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HPEITLVKVAEDQIGARVGYIEIDLNSGKILBSFRPEERPPMMSTFKVLLCGAVLSRID 60
24 HPEITLVKVAEDQIGARVGYIEIDLNSGKILBSFRPEERPPMMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIYSQNDLVESPYVTKKHLTDGMYRELCSAIIYMSDNTAAILLTTIGSP 120
DB 84 AGGQQLGRRIYSQNDLVESPYVTKKHLTDGMYRELCSAIIYMSDNTAAILLTTIGSP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDEPDTMPVAAATTLRKLLTGE 172
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIPNDEPDTMPVAAATTLRKLLTGE 195

Search completed: June 10, 2005, 10:49:12
Job time : 67.6888 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 49.9177 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149
Perfect score: 770
Sequence: 1 HPEITLVKVKQDAEDQ/GARVG.....MGDHYTRLDKWEPELNEAIP 149

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trcml:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	229	2	06WMY5 Klebsiella
2	770	100.0	232	2	06WMY4 Hafnia alve
3	770	100.0	241	2	06WMY8 Klebsiella
4	770	100.0	242	2	06WMY3 Escherichia
5	770	100.0	285	2	06KB67 hordeum vul
6	770	100.0	286	2	038058 bacterioph
7	770	100.0	286	2	000626 staphylococ
8	770	100.0	286	2	079CL6 methylobact
9	770	100.0	286	2	079DR3 Escherichia
10	769	99.9	225	2	038212 bacterioph
11	769	99.9	232	2	06PRU7 Escherichia
12	769	99.9	255	2	084H50 Escherichia
13	769	99.9	261	2	084H49 Klebsiella
14	769	99.9	264	2	06PRU6 acinetobact
15	769	99.9	281	2	06OIV0 Escherichia
16	769	99.9	282	2	06OIV1 Escherichia
17	769	99.9	286	1	BLAT_ECOLI
18	769	99.9	286	1	BLAT_SALTY
19	769	99.9	286	2	053043 Klebsiella
20	769	99.9	286	2	08KMY4 Escherichia
21	769	99.9	286	2	08KSD3 Klebsiella
22	769	99.9	286	2	08VP43 Klebsiella
23	769	99.9	286	2	093328 Escherichia
24	769	99.9	286	2	0934D7 Escherichia
25	769	99.9	286	2	093A77 Escherichia
26	769	99.9	286	2	093G13 Klebsiella
27	769	99.9	286	2	06K253 haemophilus
28	769	99.9	286	2	06IT48 Escherichia
29	769	99.9	286	2	06LBN9 pseudomonas
30	769	99.9	286	2	06LCV6 neisseria g
31	769	99.9	286	2	06SOJ9 streptococc

32	769	99.9	286	2	06TMH1 streptococc
33	769	99.9	286	2	06UVM7 acinetobact
34	769	99.9	286	2	06WJ74 Escherichia
35	769	99.9	286	2	06W9J1 enterobacte
36	769	99.9	286	2	06WRX2 zymomonas m
37	769	99.9	286	2	06WZD4 acinetobact
38	769	99.9	286	2	06ZYM6 salmonella
39	769	99.9	286	2	07B3X5 citrobacter
40	769	99.9	286	2	07B899 Klebsiella
41	769	99.9	286	2	07BP57 shigella fl
42	769	99.9	286	2	07BR75 neisseria m
43	769	99.9	286	2	07DFY3 salmonella
44	769	99.9	286	2	07DHD3 serratia ma
45	769	99.9	286	2	0844X1 klebsiella

ALIGNMENTS

RESULT 1					
ID	Q6WMY5	PRELIMINARY;	PRT;	229 AA.	
AC	Q6WMY5;				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	Beta-lactamase (Fragment).				
GN	Name=BlatEM;				
OS	Klebsiella oxyloca.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Klebsiella.				
OX	NCBI_TaxID=571;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MISC126;				
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;				
RL	Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AY265885; AAP3843.1; -				
DR	HSP; P00807; IXGE.				
DR	InterPro; IPR000871; Beta_lactamase_A.				
DR	PRINTS; PR00118; BLACTAMASEA.				
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.				
FT	NON_TER	1			
FT	NON_TER	1			
SQ	SEQUENCE 229 AA; 25067 MW; C65582C2617F4467 CRC64;				
Query Match					
100.0%; Score 770; DB 2; Length 229;					
Best Local Similarity 100.0%; Pred. No. 1,7e-62;					
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 HPEITLVKVKQDAEDQ/GARVGITIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60				
DB	2 HPEITLVKVKQDAEDQ/GARVGITIEDLNSGKILSFRRPFRPPMSTFVLLCGAVLSRID 61				
QY	61 AGQELGRHYSONDVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGSP 120				
DB	62 AGQELGRHYSONDVEYSPVTEKHLTDGMTVRELCSAIIITMSDNTAANLLTTIGSP 121				
QY	121 KEITAFILNMGDHYTRLDKWEPELNEAIP 149				
DB	122 KEITAFILNMGDHYTRLDKWEPELNEAIP 150				
RESULT 2					
ID	Q6WMY4	PRELIMINARY;	PRT;	232 AA.	
AC	Q6WMY4;				
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	Beta-lactamase (Fragment).				
GN	Name=BlatEM;				
OS	Hafnia alvei.				

```
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Hafnia.
OX NCBI_TaxID=5659;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC198;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265886; AAP93844.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 232 232
SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1,7e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVKKQAEADLGARVGIETLDNSGKILSFRRPFRPPMSTFKVLICGAVLSRID 60
D 2 HPELVVKKQAEADLGARVGIETLDNSGKILSFRRPFRPPMSTFKVLICGAVLSRID 61
QY 61 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 120
D 62 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 121
QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAIP 149
D 122 KETLAFLLHMGDHYTRLDRWEPELNEAIP 150

RESULT 3
Q6MWY8 PRELIMINARY; PRT; 241 AA.
AC Q6MWY8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
GN Name=blatEM;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC112;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265882; AAP93840.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 770; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVKKQAEADLGARVGIETLDNSGKILSFRRPFRPPMSTFKVLICGAVLSRID 60
D 7 HPELVVKKQAEADLGARVGIETLDNSGKILSFRRPFRPPMSTFKVLICGAVLSRID 66
QY 61 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 120
D 62 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 120
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D 67 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 126
QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAIP 149
D 127 KETLAFLLHMGDHYTRLDRWEPELNEAIP 155

RESULT 4
Q6MWY3 PRELIMINARY; PRT; 242 AA.
AC Q6MWY3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
GN Name=blatEM;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7A005;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY265887; AAP93845.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 26554 MW; 38CDPA8A5A3807D CRC64;

Query Match 100.0%; Score 770; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.8e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVVKKQAEADLGARVGIETLDNSGKILSFRRPFRPPMSTFKVLICGAVLSRID 60
D 8 HPELVVKKQAEADLGARVGIETLDNSGKILSFRRPFRPPMSTFKVLICGAVLSRID 67
QY 61 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 120
D 68 AGOQLGRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAALTMSDNTAANLLTTTGGP 127
QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAIP 149
D 128 KETLAFLLHMGDHYTRLDRWEPELNEAIP 156

RESULT 5
Q6KB67 PRELIMINARY; PRT; 285 AA.
AC Q6KB67;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Hordeum vulgare (Barley).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=First leaf;
RA Jansen C., Korell M., Eckey C., Biedenkopf D., Kogel K.H.;
RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ717739; CAG30723.1; -.
DR HSSP; P00807; IALQ.
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DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase_1.
DR PRINTS: PR00118; BLACTAMASEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
DR Hypothetical protein.
FT NON TER 285
SQ SEQUENCE 285 AA; 31371 MW; A2P22753375FA930 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGAVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQDAEDDQAGAVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGCP 120
DB 84 AGOQOLGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGCP 143
QY 121 KELTSAPLNMGDHVTRLDRMEPELNEAIP 149
DB 144 KELTSAPLNMGDHVTRLDRMEPELNEAIP 172

RESULT 6
Q38058 PRELIMINARY; PRT; 286 AA.
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta_lactamase.
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=95174401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
RA Henrich B., Schmidberger B.;
RT "A variant of phiX174 gene E-based positive selection vectors with
RT enhanced lytic potential.";
RL Gene 154:51-54(1995).
DR EMBL; Z35638; CAA84692.1; -.
DR PIR; S47061; S47061.
DR HSSP; Q9R435; 1HTZ.
DR InterPro: IPR000871; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGAVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQDAEDDQAGAVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGCP 120
DB 84 AGOQOLGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGCP 143
QY 121 KELTSAPLNMGDHVTRLDRMEPELNEAIP 149
DB 144 KELTSAPLNMGDHVTRLDRMEPELNEAIP 172

RESULT 7
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Q00626 PRELIMINARY; PRT; 286 AA.
ID Q00626
AC Q00626; 008022; 008102; 009393; 009396; 009397; 009398; 009399;
AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
AC 009408; 009481; 009482; 009483; 009490; 057333;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 26, Last annotation update)
DE Beta_lactamase.
OS Staphylococcus aureus.
OG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N. A.
RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
RX MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plae.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RT "The staphylococcal insertion sequence IS257 is active.";
RL Plasmid 34:198-205(1995).
DR EMBL; U36912; AA83957.1; -.
DR EMBL; U36911; AA83956.1; -.
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase_1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KM Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQDAEDDQAGAVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQDAEDDQAGAVGYIELDLSGKILSFRRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGCP 120
DB 84 AGOQOLGRRIRHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTIGCP 143
QY 121 KELTSAPLNMGDHVTRLDRMEPELNEAIP 149
DB 144 KELTSAPLNMGDHVTRLDRMEPELNEAIP 172

RESULT 8
Q79CL6 PRELIMINARY; PRT; 286 AA.
ID Q79CL6
AC Q79CL6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta_lactamase.
GN Name-bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobacterales;
OC Methylobacteriaceae; Methylobacillales.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=97074643; PubMed=891070; DOI=10.1016/0378-1119(96)00114-X;
RA Serebrijski I.G., Vasein V.M., Tsyankov Y.D.;
RT "Two new members of the BioB superfamily: cloning, sequencing and
RT expression of bioB genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum.";
RL Gene 175:15-22(1996).
RN [2]
RP SEQUENCE FROM N. A.
RA Serebrijski I., Vasein V., Tsyankov Y.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U31280; AAC44581.1; -.
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DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase_A.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKQAEADLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQAEADLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGP 143
QY 121 KETLAFIHNMGDHYTRLDRWEPEINEAIP 149
DB 144 KETLAFIHNMGDHYTRLDRWEPEINEAIP 172
RESULT 9
ID Q79DR3 PRELIMINARY; PRT; 286 AA.
AC Q79DR3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name:bla; Synonyms=blatEM-116;
OS Escherichia coli.
OC Plasmid pBP4, and plasmid pCAPS.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=PRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RL Little M., Breitling F.;
RN Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RC PLASMID=PCAP6;
RA MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RL Schleper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the cfp gene
RT Escherichia coli.";
RL Anal. Biochem. 257:203-209(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC PubMed=1524306;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey.";
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -;
DR EMBL; Y12694; CAA73226.1; -;
DR EMBL; AJ001614; CAA04868.1; -;
DR EMBL; AY425988; AA095605.1; -;

DR HSSP; P00807; 1ALQ.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase_A.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydroxylase; Plasmid; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
Query Match 100.0%; Score 770; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-62;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKQAEADLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQAEADLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGP 143
QY 121 KETLAFIHNMGDHYTRLDRWEPEINEAIP 149
DB 144 KETLAFIHNMGDHYTRLDRWEPEINEAIP 172

RESULT 10
ID Q38212 PRELIMINARY; PRT; 225 AA.
AC Q38212;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Bacteriophage phi-R208 amplicillinase gene mutation. (fragment).
OS Bacteriophage phi.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10863;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Badie J.S., Conrad M.;
RT "O-6-methylguanine mutation and repair is nonuniform. Selection for
RT DNA most interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885(1986).
DR EMBL; M14017; AAA32208.1; -;
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;
Query Match 99.9%; Score 769; DB 2; Length 225;
Best Local Similarity 99.3%; Pred. No. 2.1e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKQAEADLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQAEADLGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGP 120
DB 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGP 143
QY 121 KETLAFIHNMGDHYTRLDRWEPEINEAIP 149
DB 144 KETLAFIHNMGDHYTRLDRWEPEINEAIP 172

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RESULT 11
Q6PRU7 PRELIMINARY; PRT; 232 AA.
ID Q6PRU7
AC Q6PRU7
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U33;
RA Ghadiali S., Hoseini-Mazinan S.M.;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY583761; AAS86427.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285EE70BB0 CRC64;

Query Match 99.9%; Score 769; DB 2; Length 232;
Best Local Similarity 99.3%; Pred. No. 2,1e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 15 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 74
QY 61 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 75 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 134
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIP 149
DB 135 KETLAFILNMGDHVTIRLDREWEPELNEAIP 163

RESULT 12
Q84H50 PRELIMINARY; PRT; 255 AA.
ID Q84H50
AC Q84H50
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanhal M.A.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY130282; AAN05026.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;
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Query Match 99.9%; Score 769; DB 2; Length 255;
Best Local Similarity 99.3%; Pred. No. 2,4e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 71
QY 61 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 72 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 131
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIP 149
DB 132 KETLAFILNMGDHVTIRLDREWEPELNEAIP 160

RESULT 13
Q84H49 PRELIMINARY; PRT; 261 AA.
ID Q84H49
AC Q84H49
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanhal M.A., Verhoef J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F773A08CB8 CRC64;

Query Match 99.9%; Score 769; DB 2; Length 261;
Best Local Similarity 99.3%; Pred. No. 2,5e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVAEDQAGAVGYIEIDLSGKILSFREPERPPMSTFKVLLCGAVLSRID 71
QY 61 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 72 AGOGLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 131
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIP 149
DB 132 KETLAFILNMGDHVTIRLDREWEPELNEAIP 160

RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
ID Q6PRU6
AC Q6PRU6
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U11;
RA Chandilli S., Hoseelini-Mazinani S.M.;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY583762; AAS86428.1; -.
DR HSSP; P00807; 1A1Q.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 264 AA; 264 264
A4F071CF7489352C CRC64;

Query Match 99.9%; Score 769; DB 2; Length 264;
Best Local Similarity 99.3%; Pred. No. 2.5e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPELTIVKVDADOLGARVGYIELDLSGKILSFPRPEPRPMSTFKVLLCGAVLSRID 60
|||
12 HPELTIVKVDADOLGARVGYIELDLSGKILSFPRPEPRPMSTFKVLLCGAVLSRYD 71
|||
DB 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITWSDNTANLLTTIGSP 120
|||
72 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITWSDNTANLLTTIGSP 131
|||
OY 121 KETLAFILNMGDHYTRLDRWEPELNEAIP 149
|||
DB 132 KETLAFILNMGDHYTRLDRWEPELNEAIP 160
|||

RESULT 15

OQOIVO PRELIMINARY; PRT; 281 AA.
AC OQOIVO;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (Fragment).
GN Name=blatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; 1A1Q.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 281
FT NON TER 281
SQ SEQUENCE 281 AA; 30837 MM; C8934B9C696057BF CRC64;

Query Match 99.9%; Score 769; DB 2; Length 281;
Best Local Similarity 99.3%; Pred. No. 2.7e-62;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HPELTIVKVDADOLGARVGYIELDLSGKILSFPRPEPRPMSTFKVLLCGAVLSRID 60
|||
24 HPELTIVKVDADOLGARVGYIELDLSGKILSFPRPEPRPMSTFKVLLCGAVLSRYD 83
|||
OY 61 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITWSDNTANLLTTIGSP 120
|||

DB 84 AGQQLGRRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITWSDNTANLLTTIGSP 143
|||
OY 121 KETLAFILNMGDHYTRLDRWEPELNEAIP 149
|||
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIP 172
|||

Search completed: June 10, 2005, 10:57:01
Job time : 50.9177 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 10.8657 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_149

Perfect score: 770

Sequence: 1 HPEITLVKVKDABDQIGARVGVYIELDLNSGKILSPRPFRPMMSTFVLLCGAVLSRID

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	770	100.0	286 2 T51301	beta-lactamase (EC
2	770	100.0	286 2 S47061	beta-lactamase (EC
3	770	100.0	286 4 S41975	beta-lactamase (EC
4	769	99.9	286 1 PNECP	beta-lactamase (EC
5	769	99.9	286 4 I40905	beta-lactamase (EC
6	761	98.8	286 2 S30113	beta-lactamase (EC
7	756	98.2	286 2 S60312	extended spectrum
8	755	98.1	286 2 S60310	extended spectrum
9	755	98.1	286 2 S60311	beta-lactamase (EC
10	755	98.1	286 2 JQ1546	Bla protein - Salm
11	552	71.7	286 2 S16146	beta-lactamase (EC
12	552	71.7	286 2 A60679	beta-lactamase (EC
13	548	71.2	265 2 S00464	beta-lactamase (EC
14	548	71.2	265 2 S02434	beta-lactamase (EC
15	548	71.2	265 2 A60448	beta-lactamase (EC
16	548	71.2	286 1 A44998	beta-lactamase (EC
17	548	71.2	286 2 A60632	beta-lactamase (EC
18	548	71.2	286 2 A47200	beta-lactamase (EC
19	542	70.4	287 1 A44996	beta-lactamase (EC
20	527	68.4	279 1 A24469	beta-lactamase (EC
21	508	66.0	286 1 A44958	beta-lactamase (EC
22	406	52.7	298 2 A41381	beta-lactamase (EC
23	340.5	44.2	23 S06967	beta-lactamase (EC
24	335.5	43.6	306 1 B45822	beta-lactamase (EC
25	332	43.1	281 2 D93395	probable Beta lact
26	330.5	42.9	302 2 S36188	beta-lactamase (EC
27	330.5	42.9	306 2 G69674	beta-lactamase (EC
28	322.5	41.9	311 2 JN0520	beta-lactamase (EC
29	318.5	41.4	306 2 S47330	penicillinase - Ba

30	316.5	41.1	305 1 C45822	beta-lactamase (EC
31	312	40.5	305 2 A61156	beta-lactamase (EC
32	312	40.5	305 2 A57002	beta-lactamase (EC
33	312	40.5	305 2 A60680	beta-lactamase (EC
34	311	40.4	314 1 PMSMU	beta-lactamase (EC
35	309.5	40.2	311 1 S02714	beta-lactamase (EC
36	308.5	40.1	294 2 S16553	beta-lactamase (EC
37	307	39.9	293 2 S04649	beta-lactamase (EC
38	305.5	39.7	307 1 PMSLU	beta-lactamase (EC
39	304.5	39.5	263 2 A54543	beta-lactamase (EC
40	301.5	39.2	291 2 S42075	beta-lactamase (EC
41	301.5	39.2	306 1 PMS5B	beta-lactamase (EC
42	296.5	38.5	306 1 PMS5B	beta-lactamase (EC
43	296.5	38.5	306 2 S03167	beta-lactamase (EC
44	294	38.2	294 2 S44080	beta-lactamase (EC
45	293	38.1	310 2 J10091	beta-lactamase (EC

ALIGNMENTS

RESULT 1
T51301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C/Accession: T51301
R/WACH, A.; BRACHAT, A.; ALBERTSSEUT, C.; REBISCHUNG, C.; PHILIPPSEN, P.
Yeast 13, 1065-1075, 1997
A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A/Reference number: 209587
A/Accession: T51301
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-286 <MAC>
A/Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
A/Genetics:
A/Gene: bla
A/Superfamily: beta-lactamase I
C/Keywords: hydrolase

Query Match 100.0%; Score 770; DB 2; Length 286;
Best local similarity 100.0%; Pred. No. 1.9e-66;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDABDQIGARVGVYIELDLNSGKILSPRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKDABDQIGARVGVYIELDLNSGKILSPRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGOEQLGRIRHYSONDLVEYSPVTEKHLTDGVTYRELCSAATWSDNTAAVLLTTIGP 120
DB 84 AGOEQLGRIRHYSONDLVEYSPVTEKHLTDGVTYRELCSAATWSDNTAAVLLTTIGP 143
QY 121 KELTAFLLNMGDHVTYLRWPELNEAIP 149
DB 144 KELTAFLLNMGDHVTYLRWPELNEAIP 172

RESULT 2
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beta-lactamase (EC 3.5.2.6) - phage phi-X174
C/Species: phage phi-X174
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S47061
R/Henrich, B.; Schmidtberger, B.
Submitted to the EMBL Data Library, July 1994
A/Description: A variant of phiX174 gene E-based positive selection vectors with enhanced
A/Reference number: S47060
A/Accession: S47061
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <HEN>
A/Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g52095;

RESULT 13

beta-lactamase (BC 3.5.2.6) class A - *Escherichia coli* plasmid p453
 N/Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
 C/Species: *Escherichia coli*
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
 C/Accession: S00464
 R/Barthelemy, M.; Peduzzi, J.; Labia, R.
 Biochem. J. 251, 73-79, 1988
 A/Rtitle: Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-lactamase (SHV-1)
 A/Reference number: S00464; MUID:88268817; PMID:3260490
 A/Accession: S00464
 A/Molecule type: protein
 A/Residues: 1-265 <BAR>
 C/Genetics:
 A/Genome: plasmid
 C/Superfamily: beta-lactamase I
 C/Keywords: antibiotic resistance; hydrolase

Query Match	71.2%;	Score 548;	DB 2;	Length 265;
Best Local Similarity	70.3%;	Pred. No. 3.8e-45;		
Matches 104;	Conservative 21;	Mismatches 23;	Indels 0;	Gaps 0

QY 2 PETLVKVAEDQLGARVGYIELDNSKILLESFPEEFPMSTFKVLTCGAVLSRIDA 61
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Dd 2 PQPLEQIKUSESQLSGRVGMTEMDLASGRITLAWRADSRPFPMSTFKVLTGAVLARVDA 61

Oy 62 GGEQLGRIRIHYSQNDLVBYSPVTEKHLTDGNTVRELCSPAATMSDNTAANLLTTIGSPK 121
 | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
Db 62 GDEQLERKIHYRQDDLVDYSPVSEKHLADGNTVGELCAAAITMSDNSAANLLTAVGSPA 121

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Qy      122 ELTAFLNMGDHTRLDRWEPELNEAIP 149
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Db      122 GLTAFLRQIGDNTRLDRWETELNEALP 149

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RESULT 14

beta-lactamases (EC 3.5.2.6) SHV-2 - *Escherichia coli*
 C:Species: *Escherichia coli*
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
 C:Accession: S02434
 R:Barthelemy, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R.
 FEBS Lett. 231, 217-220, 1988
 A:Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydrolase
 A:Reference number: S02434; PMID:88196385; PMID:3129305
 A:Accession: S02434
 A:Molecule type: protein
 A:Residues: 1-265 <BAR>
 C:Superfamily: beta-lactamase I
 C:Keywords: antibiotic resistance; hydrolase

Query Match	71.2%	Score 549	DB 2:	length 265;
Best Local Similarity	70.3%	Pred. No. 3.8e-45;		
Matches 104; Conservative	21;	Mismatches 23;	Indels 0;	Gaps 0

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      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Qy	122	ELTAFLLHNGSDHYTRLDRWEPELNEALP	1499
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Ds	122	GLTAFLLRQIGDNTVRLDRWETELNEALP	1499

RESULT 15

A60448

beta-lactamase (EC 3.5.2.6) CAZ-5 - *Klebsiella pneumoniae* (strain 210-2)

C:/Species: Klebsiella pneumoniae
C:/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 16-Aug-2004
C:/Accession: A60448
C:/Reduzzi, J.; Barthélemy, M.; Tiwari, K.; Mattioni, D.; Labia, R.
Antimicrob. Agents Chemother. 33, 2160-2163, 1989
A:/Title: Structural features related to hydrolytic activity against ceftriaxime of plasmid
A:/Reference number: A60448; PMID:90146269; PMID:2694955
A:/Accession: A60448
A:/Status: preliminary
A:/Molecule type: protein
A:/Residues: 1-265 <PDB>
A:/Cross-references: UNIPROT:P37323
C:/Superfamily: Beta-lactamase I
C:/Keywords: hydrolase

Query Match	71.24;	Score 548;	DB 2;	length 265;
Best Local Similarity	70.34;	Pred. No. 38-45;		
Matches 104;	Conservative 21;	Mismatches 23;	Indels 0;	Gaps 0

Dy 2 PETLVKVKQAEADQLGARVGIETLDLNSGKILFSRPERRFPNMSTFKVLTCGAVLSRIDA 61

Dd 2 PQLLEQIKTSESQSLSGRVGIEMDLASGRITLAMRADRFPMNSTFKVVLCGAVLARVDA 61

Dy 62 GGEQLGRIRIHYSNDLVESPVTEKHLTGMTVRELCSAAITMSDNTAANLLTTGGSP 121
| | | | : | | | : | | | | : | | | : | |
Db 62 GBEQLERKIHYRDDLVDSFVSSEKHLADGMTVGELCAAITMSDNSAANULLATVGSPA 121

Qy	122	ELTAFIHNQGDVTRLDRWEPELNEAIP	145
		: : :	
Db	122	GLTAFILRQIGDNTRLDRWETELNEALP	145

Search completed: June 10, 2005, 10:58:46
Job time : 11.8657 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:16:31 ; Search time 17.6347 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPEITLVKXKAEDQLGARVG.....RDTMPVAMATTLAKLTGE 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	286	1	US-07-721-775A-2
2	885	100.0	286	1	US-06-339-658-2
3	885	100.0	286	3	US-09-263-933-7
4	885	100.0	286	3	US-09-263-933-14
5	885	100.0	286	3	US-09-263-933-21
6	885	100.0	286	3	US-09-025-769B-265
7	885	100.0	286	3	US-09-025-769B-362
8	885	100.0	286	4	US-09-919-901-7
9	885	100.0	286	4	US-09-919-901-14
10	885	100.0	286	4	US-09-919-901-21
11	885	100.0	286	4	US-09-490-070A-265
12	885	100.0	286	4	US-09-490-070A-362
13	885	100.0	286	4	US-09-490-153-265
14	885	100.0	286	4	US-09-490-153-362
15	885	100.0	286	4	US-10-191-966-7
16	885	100.0	286	4	US-10-191-966-14
17	885	100.0	286	4	US-10-191-966-21
18	885	100.0	286	4	US-09-490-324-265
19	885	100.0	286	4	US-09-490-324-362
20	885	100.0	299	3	US-09-025-769B-285
21	885	100.0	299	3	US-09-025-769B-298
22	885	100.0	299	4	US-09-025-769B-300
23	885	100.0	299	4	US-09-490-070A-285
24	885	100.0	299	4	US-09-490-070A-298
25	885	100.0	299	4	US-09-490-070A-300
26	885	100.0	299	4	US-09-490-153-285
27	885	100.0	299	4	US-09-490-153-298

28	885	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	885	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	885	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	885	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	885	100.0	2307	3	US-09-263-933-2	Sequence 2, Appl1
33	885	100.0	2307	3	US-09-263-933-9	Sequence 9, Appl1
34	885	100.0	2307	3	US-09-263-933-16	Sequence 16, Appl1
35	885	100.0	2307	4	US-09-919-901-2	Sequence 2, Appl1
36	885	100.0	2307	4	US-09-919-901-9	Sequence 9, Appl1
37	885	100.0	2307	4	US-09-919-901-16	Sequence 16, Appl1
38	885	100.0	2307	4	US-10-191-966-2	Sequence 2, Appl1
39	885	100.0	2307	4	US-10-191-966-9	Sequence 9, Appl1
40	885	100.0	2307	4	US-10-191-966-16	Sequence 16, Appl1
41	884	99.9	286	4	US-09-555-510B-9	Sequence 9, Appl1
42	884	99.9	286	4	US-10-231-013-9	Sequence 9, Appl1
43	884	99.9	1293	4	US-09-170-436D-292	Sequence 292, App
44	884	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl1
45	880	99.4	263	1	US-08-407-544-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-721-775A-2
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5180666ak, Raymond P.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Reising, Ethnington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07721,775A
; FILING DATE: 19910627
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-721-775A-2

Query Match 100.0%; Score 885; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPEITLVKXKAEDQLGARVGITIEDLNSGKTLSPREPRPMSTFVTLGAVLSRID 60
Db 24 HPEITLVKXKAEDQLGARVGITIEDLNSGKTLSPREPRPMSTFVTLGAVLSRID 83

QY 61 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAI PNDERDTMPVMAATLRLKLTGE 172
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAI PNDERDTMPVMAATLRLKLTGE 195

RESULT 2

US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Reising, Ethnington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 885; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVYKDAEDLGARVGIETDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 60
DB 24 HPEITLVYKDAEDLGARVGIETDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 83
QY 61 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAI PNDERDTMPVMAATLRLKLTGE 172
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAI PNDERDTMPVMAATLRLKLTGE 195

RESULT 3
US-09-263-933-7

Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVYKDAEDLGARVGIETDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 60
DB 24 HPEITLVYKDAEDLGARVGIETDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 83
QY 61 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAI PNDERDTMPVMAATLRLKLTGE 172
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAI PNDERDTMPVMAATLRLKLTGE 195

RESULT 4

US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVYKDAEDLGARVGIETDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 60
DB 24 HPEITLVYKDAEDLGARVGIETDLNSGKILSFREPERPMMSTFKVLICGAVLSRID 83
QY 61 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGGOLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143

QY 121 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGE 172
 DB 144 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGE 195

RESULT 5
 US-09-263-933-21

; Sequence 21, Application US/09263933
 ; Patent No. 6280940

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.
 ; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patrick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

; FILE REFERENCE: 0125-0005A

; CURRENT FILING DATE: 1999-03-08

; EARLIER APPLICATION NUMBER: 09/129,611

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

US-09-263-933-21

Query Match

Best Local Similarity 100.0%; Score 885; DB 3; Length 286;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSNGKILSFRRPFRPMSTFKYLCCGAVLSRID 60

DB 24 HPEITLVKVDADQAGAVGYIELDLSNGKILSFRRPFRPMSTFKYLCCGAVLSRID 83

QY 61 AGQEQGRRIHNSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGSP 120

DB 84 AGQEQGRRIHNSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGSP 143

QY 121 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGE 172

DB 144 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGE 195

RESULT 6
 US-09-025-769B-265

; Sequence 265, Application US/09025769B
 ; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MOREPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; INFORMATION FOR SEQ ID NO: 265:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-025-769B-265

Query Match

Best Local Similarity 100.0%; Score 885; DB 3; Length 286;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDLSNGKILSFRRPFRPMSTFKYLCCGAVLSRID 60

DB 24 HPEITLVKVDADQAGAVGYIELDLSNGKILSFRRPFRPMSTFKYLCCGAVLSRID 83

QY 61 AGQEQGRRIHNSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGSP 120

DB 84 AGQEQGRRIHNSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTANLLTTIGSP 143

QY 121 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGE 172

DB 144 KETLAFILNMGDHTVRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGE 195

RESULT 7
 US-09-025-769B-362

; Sequence 362, Application US/09025769B
 ; Patent No. 6300064

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESS:

; ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/025,769B

; FILING DATE: 18-FEB-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MOREPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

;; INFORMATION FOR SEQ ID NO: 362:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 286 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 885; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 83
QY 61 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 195

RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 7
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: ;
US-09-919-901-7

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 83
QY 61 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 195

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 14
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: ;
US-09-919-901-14

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 83
QY 61 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 195

RESULT 10
US-09-919-901-21
Sequence 21, Application US/09919901
Patent No. 6599738

;; GENERAL INFORMATION:
;; APPLICANT: Potts, Karen E.
;; APPLICANT: Jackson, Roberta L.
;; APPLICANT: Patick, Amy K.
;; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
;; FILE REFERENCE: 0125-0005A
;; CURRENT APPLICATION NUMBER: US/09/919,901
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 09/263,933
;; PRIOR FILING DATE: 1999-02-08
;; PRIOR APPLICATION NUMBER: 09/129,611
;; PRIOR FILING DATE: 1998-08-05
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 21
;; LENGTH: 286
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: ;
US-09-919-901-21

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMSFTFVLLCGAVLSRID 83
QY 61 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQQLGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWEPELNEAIPNDRDITTMVAAATTIRKLLTGE 195

Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOIGRIHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGGP 120
Db 84 AGOEOIGRIHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 172
Db 144 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 195

RESULT 11
US-09-490-070A-265
; Sequence 265, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Laming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAlliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070A-265

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOIGRIHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGGP 120
Db 84 AGOEOIGRIHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 172
Db 144 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 195

Db 144 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 195

RESULT 12
US-09-490-070A-362
; Sequence 362, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Laming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAlliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFPEERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGOEOIGRIHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGGP 120
Db 84 AGOEOIGRIHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 172
Db 144 KELITAFILNMGDHVTRLDRWEPELNEAIPNDRDITTPVAMATTLLKLTGE 195

RESULT 13
US-09-490-153-265
; Sequence 265, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265
Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITTMVAMATTIRKLITGE 172
DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITTMVAMATTIRKLITGE 195
RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362
Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPELVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPELVKVKADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 120
DB 84 AGQELGRIRHYSQNDLYEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITTMVAMATTIRKLITGE 172
DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDITTMVAMATTIRKLITGE 195
RESULT 15
US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPLICATOR GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.7e-96;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HPETLVKVDADSDQAGARVGYIELDINSKILESFRPERFPWMSTFKYLCAVLSRID	60
Db	24	HPETLVKVDADSDQAGARVGYIELDINSKILESFRPERFPWMSTFKYLCAVLSRID	83
Qy	61	AGQEOIGRRIRHYSQNDLVEYSPYTEKHLTDGMTVRELCSAITMSDNTANILLTTIGSP	120
Db	84	AGQEOIGRRIRHYSQNDLVEYSPYTEKHLTDGMTVRELCSAITMSDNTANILLTTIGSP	143
Qy	121	KELTAFLEHMGDHYTRLDRWEPPELNEAIPNDERDITMPVAMATTILKLLTGE	172
Db	144	KELTAFLEHMGDHYTRLDRWEPPELNEAIPNDERDITMPVAMATTILKLLTGE	195

Search completed: June 10, 2005, 11:01:15
Job time : 18.6347 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 12.543 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPETLVKVKQADBDQGAHV...RDTPVPMATYLRRLNGE 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	286	2	TS1301
2	885	100.0	286	2	beta-lactamase (EC
3	885	100.0	286	4	beta-lactamase (EC
4	880	99.4	286	1	beta-lactamase (EC
5	880	99.4	286	4	beta-lactamase (EC
6	872	98.5	286	2	beta-lactamase (EC
7	867	98.0	286	2	beta-lactamase (EC
8	866	97.9	286	2	beta-lactamase (EC
9	866	97.9	286	2	beta-lactamase (EC
10	866	97.9	286	2	beta-lactamase (EC
11	868	71.0	286	2	beta-lactamase (EC
12	868	71.0	286	2	beta-lactamase (EC
13	862	70.5	265	2	beta-lactamase (EC
14	862	70.5	265	2	beta-lactamase (EC
15	862	70.5	265	2	beta-lactamase (EC
16	862	70.5	265	2	beta-lactamase (EC
17	862	70.5	286	2	beta-lactamase (EC
18	862	70.5	286	2	beta-lactamase (EC
19	863	68.1	279	2	beta-lactamase (EC
20	599.5	67.7	287	1	beta-lactamase (EC
21	573	64.7	286	1	beta-lactamase (EC
22	482	54.5	298	2	beta-lactamase (EC
23	392.5	44.4	281	2	beta-lactamase (EC
24	382.5	43.2	314	2	beta-lactamase (EC
25	379.5	42.9	294	2	beta-lactamase (EC
26	379.5	42.9	302	2	beta-lactamase (EC
27	378	42.7	293	2	beta-lactamase (EC
28	374.5	42.3	263	2	beta-lactamase (EC
29	371.5	42.0	291	2	beta-lactamase (EC

30	370.5	41.9	306	1	B45822	beta-lactamase (EC
31	366.5	41.4	306	2	G69674	beta-lactamase (EC
32	366.5	41.4	311	2	JN0520	beta-lactamase (EC
33	360	40.7	305	2	A61156	beta-lactamase (EC
34	360	40.7	305	2	A57002	beta-lactamase (EC
35	360	40.7	305	2	A60680	beta-lactamase (EC
36	357.5	40.4	306	2	S47330	beta-lactamase (EC
37	350.5	39.6	288	2	J01136	beta-lactamase (EC
38	350.5	39.6	291	2	JP0074	beta-lactamase (EC
39	349.5	39.5	305	1	C45822	beta-lactamase (EC
40	349	39.4	294	2	S44080	beta-lactamase (EC
41	347.5	39.3	263	2	S23929	beta-lactamase (EC
42	346.5	39.2	304	2	A49789	beta-lactamase (EC
43	346.5	39.2	304	2	A35001	beta-lactamase (EC
44	345.5	39.0	311	1	S02714	beta-lactamase (EC
45	345	39.0	314	1	PMSM1U	beta-lactamase (EC

ALIGNMENTS

RESULT 1

TS1301 beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000

C/Accession: TS1301

R/WACH, A.; BRACHAT, A.; ALBERTSSEUT, C.; REBISCHUNG, C.; PHILIPPSEN, P.

Yeast 13, 1065-1075, 1997

A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharom

A/Reference number: Z09587

A/Accession: TS1301

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-286 <MAC>

A/Cross-references: EMBL:AJ002683; PIDN:CAA05686.1

C/Genetics:

A/Gene: bla

C/Superfamily: beta-lactamase I

C/Keywords: hydrolase

Query Match 100.0%; Score 885; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 4.1e-74;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKQADBDQGAHVGIETDLSGKILIESFRPEPRPMMSTFVLLCGAVLSRID 60

DB 24 HPETLVKVKQADBDQGAHVGIETDLSGKILIESFRPEPRPMMSTFVLLCGAVLSRID 83

QY 61 AGQELGRIRIYSDNDLVESPVYTKKLTIDGTYVRELCSAATMSDNRANLLTTGGP 120

DB 84 AGQELGRIRIYSDNDLVESPVYTKKLTIDGTYVRELCSAATMSDNRANLLTTGGP 143

QY 121 KELTAFANMGDHYTRLDREPELNEALPNDERDTTVMVAAATTKLLTGE 172

DB 144 KELTAFANMGDHYTRLDREPELNEALPNDERDTTVMVAAATTKLLTGE 195

RESULT 2

S47061 beta-lactamase (EC 3.5.2.6) - phage phi-X174

C/Species: phage phi-X174

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S47061

R/Henrich, B.; Schmidtberger, B.

submitted to the EMBL Data Library, July 1994

A/Description: A variant of phix174 gene B-based positive selection vectors with enhanced

A/Reference number: S47060

A/Accession: S47061

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-286 <HEN>

A/Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g52095;

C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 100.0%; Score 885; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 172; Conservative 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGVGYIELDINSKILIESFRPERPFMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGVGYIELDINSKILIESFRPERPFMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSNDNTAANILLTTIGCP 120
DB 84 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSNDNTAANILLTTIGCP 143
QY 121 KELTSFLNMGDHTRLDRWPELNEALPNDERDITMPVAMATTLTKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWPELNEALPNDERDITMPVAMATTLTKLLTGE 195

RESULT 3

S41975
beta-lactamase (EC 3.5.2.6) precursor - synthetic

C:Species: synthetic

C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000

C:Accession: S41975

R:Kaeßter, K.H.; Montolio, L.; Kern, H.; Thulke, M.; Schütz, G.

Gene 148, 67-70, 1994

A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar

A:Reference number: A57991; MUID:95011660; PMID:7926839

A:Accession: S41975

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-286 <KAB>

A:Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623

A:Note: submitted to the EMBL Data Library, December 1993

C:Keywords: hydrolase

Query Match 100.0%; Score 885; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGVGYIELDINSKILIESFRPERPFMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGVGYIELDINSKILIESFRPERPFMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSNDNTAANILLTTIGCP 120
DB 84 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSNDNTAANILLTTIGCP 143
QY 121 KELTSFLNMGDHTRLDRWPELNEALPNDERDITMPVAMATTLTKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWPELNEALPNDERDITMPVAMATTLTKLLTGE 195

RESULT 4

PRECEP

beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids

N:Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase

C:Species: Escherichia coli

C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005

R:Sutcliffe, J.G.

Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978

A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasm

A:Reference number: A93821; MUID:79012484; PMID:358200

A:Accession: A93821

A:Molecule type: DNA

A:Residues: 1-286 <SUT>

A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:g43710; PIDN:CAA33886.1; F

A:Experimental source: plasmid pBR322

R:Ambler, R.P.; Scott, G.K.

Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978

A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid I
A:Reference number: A93820; MUID:79012483; PMID:358199

A:Accession: A93820

A:Molecule type: protein

A:Residues: 24-36, 'K', 38-286 <AMB>

A:Experimental source: plasmid R6K

R:Kornacker, J.A.; Burlage, R.S.; Figurski, D.H.

J. Bacteriol. 172, 3040-3050, 1990

A:Title: The *kil*-kor region of broad-host-range plasmid RK2: nucleotide sequence, polype

A:Reference number: A35387; MUID:90264294; PMID:2160936

A:Accession: A35387

A:Molecule type: DNA

A:Residues: 182-286 <KOR>

A:Cross-references: GB:M2794; NID:G152521; PIDN:AAA26408.1; PID:G152522

A:Experimental source: PK2

R:Gunsberg, S.; Sougkoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.

J. Gen. Microbiol. 137, 2681-2687, 1991

A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum

A:Reference number: S24415; MUID:92166702; PMID:1665171

A:Accession: S24415

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>

A:Cross-references: EMBL:X57972; NID:G41816; PIDN:CAA41038.1; PID:G41817

A:Experimental source: ISI-like blaT-6 DNA

R:Sutcliffe, J.G.

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.

A:Reference number: A90923; MUID:80002802; PMID:383387

A:Contents: annotation

C:Comment: Like most penicillinases from gram-negative bacteria, this enzyme, coded by a

C:Genetics:

A:Genome: plasmid

C:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein

F:1-33/Domains: signal sequence #status predicted <SIG>

F:24-286/Product: beta-lactamase #status experimental <MAT>

F:68/Active site: Ser #status predicted

F:75-121/Disulfide bonds: #status predicted

Query Match 99.4%; Score 880; DB 1; Length 286;
Best Local Similarity 98.8%; Pred. No. 1.2e-73;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGVGYIELDINSKILIESFRPERPFMMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGVGYIELDINSKILIESFRPERPFMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSNDNTAANILLTTIGCP 120
DB 84 AGOQLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSNDNTAANILLTTIGCP 143
QY 121 KELTSFLNMGDHTRLDRWPELNEALPNDERDITMPVAMATTLTKLLTGE 172
DB 144 KELTSFLNMGDHTRLDRWPELNEALPNDERDITMPVAMATTLTKLLTGE 195

RESULT 5

140905

beta-lactamase (EC 3.5.2.6) - synthetic

C:Species: synthetic

A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. cynod

C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000

C:Accession: 140905

R:Raylor, J.; Stearman, R.S.; Uratani, B.B.

Plasmid 29, 241-244, 1993

A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp. c

A:Reference number: 140904; MUID:93361581; PMID:7689234

A:Accession: 140905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <RES>

A:Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958

C:Keywords: hydrolase

Query Match 99.4%; Score 880; DB 4; Length 286;
Best Local Similarity 98.8%; Pred. No. 1.2e-73;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
|||||
DB 24 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
DB 84 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 172
|||||
DB 144 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 195

RESULT 6

S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - Klebsiella pneumoniae plasmid pCFP04

C:Species: Klebsiella pneumoniae
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30113
R:Chanal, C.; Lourenco-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple
A:Reference number: S30112; MUID:93062798; PMID:1331747
A:Accession: S30113
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>

A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PIDN:CAA45828.1; PID:g43798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase

Query Match 98.5%; Score 872; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 6.6e-73;
Matches 168; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
|||||
DB 24 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
DB 84 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 172
|||||
DB 144 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 195

RESULT 7

S60312
extended spectrum beta-lactamase CAZ-7 - Klebsiella pneumoniae

C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:g296955; PIDN:CAA46346.1; PID:g296956
C:Superfamily: beta-lactamase I

Query Match 98.0%; Score 867; DB 2; Length 286;
Best Local Similarity 97.1%; Pred. No. 1.9e-72;
Matches 167; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
|||||
DB 24 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
DB 84 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 172
|||||
DB 144 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 195

RESULT 8

S60310
extended spectrum beta-lactamase CAZ-2 - Klebsiella pneumoniae

C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60310
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60310
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65252; NID:g296951; PIDN:CAA46344.1; PID:g296952
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 866; DB 2; Length 286;
Best Local Similarity 97.1%; Pred. No. 2.3e-72;
Matches 167; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
|||||
DB 24 HETLVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
|||||
DB 84 AGOEOLGRRIRHSQNDLVKYSPTTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 172
|||||
DB 144 KELTAFILNMGDHVTRLDRWPEBELNEAIPNDRDRTTMPAAMATTLRKLLTGE 195

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331

C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60311; F37392; PQ0498
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60311
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>

A:Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g296954
R:Chanal, M.E.
Plasmid 24, 218-226, 1990
A:Title: Sequencing and expression of aac, bla, and tnpR from the multiresistance transi
A:Reference number: A37392; MUID:91172904; PMID:1963948
A:Accession: F37392
A:Molecule type: DNA

A:Residues: 1-32 <TOL>
A:Cross-references: GB:M55547, NID:g155010, PIDN:AAA9408.1, PID:g155016
C:Genetics:
A:Gene: TBM-bla
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance, hydrolyase

Query Match 97.9%; Score 866; DB 2; Length 286;
Best Local Similarity 97.1%; Pred. No. 2.3e-72;
Matches 167; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYELDLSNGKILIESFRPERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGRVGYELDLSNGKILIESFRPERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KETLAFINMGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 172
DB 144 KETLAFINMGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 195

RESULT 10
J01546
Bla protein - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: J01546
R:Cannon, P.M.; Striike, P.
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: J01536; MUID:9238313; PMID:1325061
A:Accession: J01546
A:Status: translation not shown
A:Residues: 1-286 <CAN>
A:Molecule type: DNA
A:Cross-references: UNIPROT:O8L2F9
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 866; DB 2; Length 286;
Best Local Similarity 97.7%; Pred. No. 2.3e-72;
Matches 168; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGRVGYELDLSNGKILIESFRPERFPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVDADQAGRVGYELDLSNGKILIESFRPERFPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 120
DB 84 AGQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KETLAFINMGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 172
DB 144 KETLAFINMGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 195

RESULT 11
S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmide
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146; A35395; S18767
R:Podbielski, A.; Schoenling, J.; Melzer, B.; Warmatz, K.; Leusch, H.G.
J:Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV-2A)
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146

A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817, NID:g43795; PIDN:CAA37813.1, PID:g43796
A:Experimental source: plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J: Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A35395; MUID:90264317; PMID:2160941
A:Accession: A35395
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LEE>
A:Cross-references: GB:X62115, NID:g48988; PIDN:CAA44025.1, PID:g48990
A:Experimental source: plasmid BWH7
C:Genetics:
A:Gene: blaS2A
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance, hydrolyase

Query Match 71.0%; Score 628; DB 2; Length 286;
Best Local Similarity 69.6%; Pred. No. 2.1e-50;
Matches 119; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

QY 2 PETLVKVDADQAGRVGYELDLSNGKILIESFRPERFPMMSTFKVLLCGAVLSRID 61
DB 23 PQLPQIRKQSSQSLSGRVGMIEMDLASGRITLTAWRADRFPMSTFKVLLCGAVLSRID 82
QY 62 GQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 121
DB 83 GQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 142
QY 122 ELTAFINMGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 172
DB 143 GLTAFIRQIGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 193

RESULT 12
A60679
beta-lactamase (EC 3.5.2.6) SHV-2 precursor - Salmonella typhimurium plasmid pHT1
C:Species: Salmonella typhimurium
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C:Accession: A60679
R:Garbary-Chenon, A.; Godard, V.; Labia, R.; Nicolaie, J.C.
Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A:Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A:Reference number: A60679; MUID:90351141; PMID:2201259
A:Accession: A60679
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <GAR>
A:Cross-references: GB:I47119, NID:g972890; PIDN:AAA75015.1, PID:g972891
C:Genetics:
A:Gene: plasmid
C:Superfamily: Beta-lactamase I
C:Keywords: antibiotic resistance, hydrolyase
F:1-21/Domain: signal sequence #status predicted <SIG>

Query Match 71.0%; Score 628; DB 2; Length 286;
Best Local Similarity 69.6%; Pred. No. 2.1e-50;
Matches 119; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

QY 2 PETLVKVDADQAGRVGYELDLSNGKILIESFRPERFPMMSTFKVLLCGAVLSRID 61
DB 23 PQLPQIRKQSSQSLSGRVGMIEMDLASGRITLTAWRADRFPMSTFKVLLCGAVLSRID 82
QY 62 GQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 121
DB 83 GQEQGRIRIHSQNDLVYSPVTEKHLLTDGNTVRELCSAATMSDNTAANLLTTIGGP 142
QY 122 ELTAFINMGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 172
DB 143 GLTAFIRQIGDHYTRLDRWPEPELNEAIPNDRDITTPMAATTKKLLTGE 193

RESULT 13

beta-lactamases (EC 3.5.2.6) class A - Escherichia coli plasmid p453
 N:Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
 C:Species: Escherichia coli
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
 C/Accession: S00464
 R:Barthelémy, M.; Peduzzi, J.; Labia, R.
 Biochem. J. 251, 73-79, 1988
 A:/Title: Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-lactamase (SHV-1)
 A:/Reference number: S00464; MUID:88268817; PMID:3260490
 A:/Accession: S00464
 A:/Molecule type: protein
 A:/Residues: 1-265 <BAR>
 C:/Genetics:
 A:/Genome: plasmid
 C:/Superfamily: beta-lactamase I
 C:/Keywords: antibiotic resistance; hydrolase

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 57.6231 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_172

Perfect score: 885
Sequence: 1 HPEITLVKVKYDADQAGARVG.....RDTWPMVAMATTIRKLITGE 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_03:*

1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	229	2	06WMY5 Klebsiella
2	885	100.0	232	2	06WMY4 Klebsiella
3	885	100.0	241	2	06WMY8 Klebsiella
4	885	100.0	242	2	06WMY3 Klebsiella
5	885	100.0	285	2	06KRB7 hordium vul
6	885	100.0	286	2	038058 bacterioph
7	885	100.0	286	2	000626 staphylococ
8	885	100.0	286	2	079CL6 methylobact
9	885	100.0	286	2	079DR3 escherichia
10	880	99.4	225	2	038212 bacterioph
11	880	99.4	232	2	06PRU7 escherichia
12	880	99.4	255	2	084H50 escherichia
13	880	99.4	261	2	084H49 escherichia
14	880	99.4	264	2	06PRU6 acinetobact
15	880	99.4	281	2	06QIV0 serratia ma
16	880	99.4	282	2	06QIV1 serratia ma
17	880	99.4	286	1	BLAT_ECOLI
18	880	99.4	286	1	BLAT_SALTI
19	880	99.4	286	2	053043 Klebsiella
20	880	99.4	286	2	08KSD3 Klebsiella
21	880	99.4	286	2	08VPA3 Klebsiella
22	880	99.4	286	2	08VPA3 Klebsiella
23	880	99.4	286	2	0934D7 escherichia
24	880	99.4	286	2	0934D7 escherichia
25	880	99.4	286	2	0934D7 escherichia
26	880	99.4	286	2	06A253 haemophilus
27	880	99.4	286	2	06LBN9 pseudomonas
28	880	99.4	286	2	06LBN9 pseudomonas
29	880	99.4	286	2	06LBN9 pseudomonas
30	880	99.4	286	2	06LBN9 pseudomonas
31	880	99.4	286	2	06W7J4 escherichia

32	880	99.4	286	2	06W9J1 enterobacte
33	880	99.4	286	2	06WRX2 zymomonas m
34	880	99.4	286	2	06WZD4 acinetobact
35	880	99.4	286	2	07B3X5 citrobacter
36	880	99.4	286	2	07B899 klebsiella
37	880	99.4	286	2	07BP57 shigella fl
38	880	99.4	286	2	07BR75 neisseria m
39	880	99.4	286	2	07DFY3 salmonella
40	880	99.4	286	2	07DHD3 serratia ma
41	880	99.4	286	2	0844X1 Klebsiella
42	880	99.4	286	2	08GA85 escherichia
43	880	99.4	286	2	09EYX1 escherichia
44	880	99.4	286	2	09K582 Klebsiella
45	880	99.4	286	2	09R770 escherichia

ALIGNMENTS

RESULT 1

ID	Query Match	Score	DB 2	Length	229
06WMY5	Best Local Similarity	100.0%	Score 885	DB 2	Length 229
06WMY5	Matches 172; Conservative	0	Mismatches 0	Indels 0	Gaps 0
AC	06WMY5	PRELIMINARY;	PRT;	229 AA.	
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	Beta-lactamase (Fragment).				
GN	Name=blatw;				
OS	Klebsiella oxytoca.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Klebsiella.				
OX	NCBI_TaxId=571;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MISC126;				
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;				
RL	Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY265885; AAP3843.1; ..				
DR	HSP; P00807; IKGE.				
DR	InterPro; IPR000871; Beta_lactamase_A.				
DR	PRINTS; PR00118; BLACTAMASEA.				
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.				
FT	NON_TER	1			
FT	NON_TER	1			
SQ	SEQUENCE	229 AA;	25067 MM;	C85582C2617F4467 CRC64;	
QY	Query Match	100.0%	Score 885	DB 2	Length 229
QY	Best Local Similarity	100.0%	Score 885	DB 2	Length 229
QY	Matches 172; Conservative	0	Mismatches 0	Indels 0	Gaps 0
QY	1 HPEITLVKVKYDADQAGARVGITELDNLGKILSFRRPFRPMNSTFKYLICGAVLSRID 60				
DB	2 HPEITLVKVKYDADQAGARVGITELDNLGKILSFRRPFRPMNSTFKYLICGAVLSRID 61				
QY	61 AGQELGRIRHYSDVLEYSPTVEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120				
DB	62 AGQELGRIRHYSDVLEYSPTVEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 121				
QY	121 KETLTFALNMGDHYTRLDWPEPELNEALPNDERDITWPMVAMATTIRKLITGE 172				
DB	122 KETLTFALNMGDHYTRLDWPEPELNEALPNDERDITWPMVAMATTIRKLITGE 173				
RESULT 2					
ID	06WMY4	PRELIMINARY;	PRT;	232 AA.	
AC	06WMY4	PRELIMINARY;	PRT;	232 AA.	
DT	05-JUL-2004 (TREMBLrel. 27, Created)				
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DR	Beta-lactamase (Fragment).				
GN	Name=blatw;				
OS	Hafnia alvei.				

```
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Hafnia.
OX NCBI_Taxid=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC138;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY265886; AAP3844.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR000871; Beta_lactamase_A.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.7e-69;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGRVGYIELDINSKLTESFRPERPPMSTFVYLCAVLSRID 60
DB 2 HPELVKVKADBDQAGRVGYIELDINSKLTESFRPERPPMSTFVYLCAVLSRID 61
QY 61 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGTVRELCSAITSNDTANILLTTIGSP 120
DB 62 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGTVRELCSAITSNDTANILLTTIGSP 121
QY 121 KELTAFLLHMGDHYTRLDRLRWEPELNEAIPNDRDITTMVMAATTLRKLTGS 172
DB 122 KELTAFLLHMGDHYTRLDRLRWEPELNEAIPNDRDITTMVMAATTLRKLTGS 173

RESULT 3
Q6MWY8 PRELIMINARY; PRT; 241 AA.
ID Q6MWY8;
AC Q6MWY8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
DE Name=blatEM;
GN Klebsiella pneumoniae.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_Taxid=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC112;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY265887; AAP3840.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR00146; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 885; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 3.8e-69;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
DB 67 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGTVRELCSAITSNDTANILLTTIGSP 126
QY 121 KELTAFLLHMGDHYTRLDRLRWEPELNEAIPNDRDITTMVMAATTLRKLTGS 172
DB 127 KELTAFLLHMGDHYTRLDRLRWEPELNEAIPNDRDITTMVMAATTLRKLTGS 178

RESULT 4
Q6MWY3 PRELIMINARY; PRT; 242 AA.
ID Q6MWY3;
AC Q6MWY3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Beta-lactamase (Fragment).
DE Name=blatEM;
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TA005;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY265887; AAP3845.1; -.
DR HSSP; P00807; IKGE.
DR InterPro; IPR00146; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 885; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.8e-69;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGRVGYIELDINSKLTESFRPERPPMSTFVYLCAVLSRID 60
DB 8 HPELVKVKADBDQAGRVGYIELDINSKLTESFRPERPPMSTFVYLCAVLSRID 67
QY 61 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGTVRELCSAITSNDTANILLTTIGSP 120
DB 68 AGOELGRIRIHYSONDLVEYSPVTEKHLTDGTVRELCSAITSNDTANILLTTIGSP 127
QY 121 KELTAFLLHMGDHYTRLDRLRWEPELNEAIPNDRDITTMVMAATTLRKLTGS 172
DB 128 KELTAFLLHMGDHYTRLDRLRWEPELNEAIPNDRDITTMVMAATTLRKLTGS 179

RESULT 5
Q6KB67 PRELIMINARY; PRT; 285 AA.
ID Q6KB67;
AC Q6KB67;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
DE Hordeum vulgare (Barley).
OS Hordeum vulgare; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_Taxid=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=First leaf;
RA Jansen C., Korell M., Beckey C., Biedenkopf D., Kogel K.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ717739; CAG30723.1; -.
DR HSSP; P00807; IALQ.
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DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 DR Hypothetical protein.
 KW NON TER 285
 FT SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 4.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMWSTFKYLICGAVLSRID 60
 DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMWSTFKYLICGAVLSRID 83
 QY 61 AGQEQGRRIRHYSQNDLYEYSPVTEKHLTDGNTVELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQEQGRRIRHYSQNDLYEYSPVTEKHLTDGNTVELCSAATMSDNTANILLTTIGSP 143
 QY 121 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITMPVAMATTIRKLLTGE 172
 DB 144 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITMPVAMATTIRKLLTGE 195

RESULT 6

Q38058 PRELIMINARY; PRT; 286 AA.

AC Q38058;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DS Beta_lactamase.
 GN Name=bla;
 OS Bacteriophage phi-X174.
 OC Viruses; ssDNA viruses; Microviridae; Microvirinae.
 CX NCBI_TaxID=10847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
 RA Henrich B., Schmidtberger B.;
 RT "A variant of phiX174 gene E-based positive selection vectors with
 enhanced lytic potential.";
 RL Gene 154:51-54 (1995).
 DR EMBL; Z35638; CAAB4692.1; -.
 DR PIR; S47061; S47061.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 DR SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 4.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMWSTFKYLICGAVLSRID 60
 DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMWSTFKYLICGAVLSRID 83
 QY 61 AGQEQGRRIRHYSQNDLYEYSPVTEKHLTDGNTVELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQEQGRRIRHYSQNDLYEYSPVTEKHLTDGNTVELCSAATMSDNTANILLTTIGSP 143
 QY 121 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITMPVAMATTIRKLLTGE 172
 DB 144 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITMPVAMATTIRKLLTGE 195

RESULT 7

000626

ID 000626 PRELIMINARY; PRT; 286 AA.
 AC 000626; 008022; 008102; 009393; 009396; 009397; 009398; 009399;
 AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
 AC 009408; 009481; 009482; 009483; 009490; 057339;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Beta_lactamase.
 OS Staphylococcus aureus.
 OG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
 RX MEDLINE=9642275; PubMed=8825372; DOI=10.1006/plas.1995.0005;
 RA Needham C., Noble W.C., Dyke K.G.;
 RT "The staphylococcal insertion sequence IS257 is active.";
 RL Plasmid 34:198-205 (1995).
 DR EMBL; U36912; AAB39957.1; -.
 DR EMBL; U36911; AAB39956.1; -.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 885; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 4.7e-69;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMWSTFKYLICGAVLSRID 60
 DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMWSTFKYLICGAVLSRID 83
 QY 61 AGQEQGRRIRHYSQNDLYEYSPVTEKHLTDGNTVELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQEQGRRIRHYSQNDLYEYSPVTEKHLTDGNTVELCSAATMSDNTANILLTTIGSP 143
 QY 121 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITMPVAMATTIRKLLTGE 172
 DB 144 KELITAFILNMGDHVTRLDRMBEPLNEAIPNDRDITMPVAMATTIRKLLTGE 195

RESULT 8

Q79CL6 PRELIMINARY; PRT; 286 AA.

AC Q79CL6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DS Beta_lactamase.
 GN Name=bla;
 OS Methylobacillus flagellatum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Methylobacterales;
 OC Methylobacteriaceae; Methylobacillus.
 CX NCBI_TaxID=405;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
 RA Seebrijski I.G., Vassin V.M., Tsygankov Y.D.;
 RT "Two new members of the BioB superfamily: cloning, sequencing and
 expression of bioB genes of Methylobacillus flagellatum and
 Corynebacterium glutamicum.";
 RL Gene 175:15-22 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Seebrijski I., Vassin V., Tsygankov Y.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U31280; AAC44501.1; -.


```

RESULT 11
Q6PRU7 PRELIMINARY; PRT; 232 AA.
ID Q6PRU7
AC Q6PRU7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=03;
RA Ghandili S., Hosseini-Mazinani S.M.;
RL Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583761; NAS86427.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285E70B80 CRC64;

Query Match 99.4%; Score 880; DB 2; Length 232;
Best Local Similarity 98.8%; Pred. No. 1e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQIGARVGYIELDINSKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
DB 15 HPEITLVKVDADQIGARVGYIELDINSKILSFPRPERFPMWSTFKVLLCGAVLSRYD 74
QY 61 AGOEQUGRIHYSQNDLVYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 75 AGOEQUGRIHYSQNDLVYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 134
QY 121 KELTAFIHNMGDHYTRLDKWEPELNEAIPNDRDITTPVAMATTAKLTGE 172
DB 135 KELTAFIHNMGDHYTRLDKWEPELNEAIPNDRDITTPVAMATTAKLTGE 186

RESULT 12
Q84H50 PRELIMINARY; PRT; 255 AA.
ID Q84H50
AC Q84H50;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanHall M.A.;
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130282; AAN05026.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PR00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B5978C3A6 CRC64;

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Query Match 99.4%; Score 880; DB 2; Length 255;
Best Local Similarity 98.8%; Pred. No. 1e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQIGARVGYIELDINSKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVDADQIGARVGYIELDINSKILSFPRPERFPMWSTFKVLLCGAVLSRYD 71
QY 61 AGOEQUGRIHYSQNDLVYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 72 AGOEQUGRIHYSQNDLVYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 131
QY 121 KELTAFIHNMGDHYTRLDKWEPELNEAIPNDRDITTPVAMATTAKLTGE 172
DB 132 KELTAFIHNMGDHYTRLDKWEPELNEAIPNDRDITTPVAMATTAKLTGE 183

RESULT 13
Q84H49 PRELIMINARY; PRT; 261 AA.
ID Q84H49
AC Q84H49;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanHall M.A., Verhoef J., Fluit A.C.;
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PR00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F733A08CB8 CRC64;

Query Match 99.4%; Score 880; DB 2; Length 261;
Best Local Similarity 98.8%; Pred. No. 1e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQIGARVGYIELDINSKILSFPRPERFPMWSTFKVLLCGAVLSRID 60
DB 12 HPEITLVKVDADQIGARVGYIELDINSKILSFPRPERFPMWSTFKVLLCGAVLSRYD 71
QY 61 AGOEQUGRIHYSQNDLVYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 72 AGOEQUGRIHYSQNDLVYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 131
QY 121 KELTAFIHNMGDHYTRLDKWEPELNEAIPNDRDITTPVAMATTAKLTGE 172
DB 132 KELTAFIHNMGDHYTRLDKWEPELNEAIPNDRDITTPVAMATTAKLTGE 183

RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
ID Q6PRU6
AC Q6PRU6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM beta-lactamase (Fragment).
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U1;
RA Chanditi S., Hosseini-Mazinani S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY563762; AAS6428.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 264 AA; 264 264
AAAF071CF7489352C CRC64;

```

```

Query Match 99.4%; Score 880; DB 2; Length 264;
Best Local Similarity 98.8%; Pred. No. 1.2e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 HPETLVKVDADQAGARVGYEILDNSKILSFRRPRPPMSTFKYLGGAVLSRID 60
DB 12 HPETLVKVDADQAGARVGYEILDNSKILSFRRPRPPMSTFKYLGGAVLSRVD 71
OY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 120
DB 72 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 131
OY 121 KETLFLNMGDHVTRLDRWEPELNEALPNDERDTMPAAMATTLRKLTGE 172
DB 132 KETLFLNMGDHVTRLDRWEPELNEALPNDERDTMPAAMATTLRKLTGE 183

```

RESULT 15

```

OQ0IV0 PRELIMINARY; PRT; 281 AA.
AC OQ0IV0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (Fragment).
GN Name=blatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 281
FT TER 281
SQ SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;

```

```

Query Match 99.4%; Score 880; DB 2; Length 281;
Best Local Similarity 98.8%; Pred. No. 1.3e-68;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

OY 1 HPETLVKVDADQAGARVGYEILDNSKILSFRRPRPPMSTFKYLGGAVLSRID 60
DB 24 HPETLVKVDADQAGARVGYEILDNSKILSFRRPRPPMSTFKYLGGAVLSRVD 83
OY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 120

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DB 84 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATWSDNTAANLLTTIGSP 143
OY 121 KETLFLNMGDHVTRLDRWEPELNEALPNDERDTMPAAMATTLRKLTGE 172
DB 144 KETLFLNMGDHVTRLDRWEPELNEALPNDERDTMPAAMATTLRKLTGE 195

```

```

Search completed: June 10, 2005, 10:57:02
Job time : 58.6231 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:22:36 ; Search time 70.1783 Seconds

(without alignments)
997.510 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925

Sequence: 1 HPETLVKVKMDQADQLGARGV.....ATTAKLKLGTGLTASRQ 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	925	100.0	263	4	AAE05544 E. coli m
2	925	100.0	263	4	AAE05544 E. coli m
3	925	100.0	263	8	ADJ67709 Escherich
4	925	100.0	264	2	AAW16634 Beta-lact
5	925	100.0	264	2	AAW18680 Intercell
6	925	100.0	264	2	AAW18680 Intercell
7	925	100.0	266	2	AAW18680 Intercell
8	925	100.0	266	2	AAW18680 Intercell
9	925	100.0	266	2	AAW18680 Intercell
10	925	100.0	266	2	AAW18680 Intercell
11	925	100.0	266	2	AAW18680 Intercell
12	925	100.0	266	2	AAW18680 Intercell
13	925	100.0	266	2	AAW18680 Intercell
14	925	100.0	266	2	AAW18680 Intercell
15	925	100.0	266	2	AAW18680 Intercell
16	925	100.0	266	2	AAW18680 Intercell
17	925	100.0	266	2	AAW18680 Intercell
18	925	100.0	266	2	AAW18680 Intercell
19	925	100.0	266	2	AAW18680 Intercell
20	925	100.0	266	2	AAW18680 Intercell
21	925	100.0	266	2	AAW18680 Intercell
22	925	100.0	266	2	AAW18680 Intercell
23	925	100.0	266	2	AAW18680 Intercell
24	925	100.0	266	2	AAW18680 Intercell
25	925	100.0	266	2	AAW18680 Intercell

ALIGNMENTS

RESULT 1	ID	AAE05544	standard; protein, 263 AA.
AC	XX	AAE05544;	
DT	XX	24-SEP-2001	(first entry)
DE	XX	E. coli mature TEM-1 beta-lactamase.	
KM	XX	Interaction-dependent enzyme association; IDBA system; biosensor;	
KW	XX	circularly permuted interaction-activated protein; marker protein;	
KW	XX	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;	
KW	XX	therapeutic; drug screening; thiolethoxin; ampicillin resistance.	
OS	XX	Escherichia coli.	
FT	FT	Key	Location/Qualifiers
FT	FT	Cleavage-site	27..28 /note="Break-point between alpha and omega fragments"
FT	FT	Region	36..40 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	38..39 /note="Inter-sub-domain loop"
FT	FT	Active-site	45 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	74..75 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	149..150 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	172..173 /note="Break-point between alpha and omega fragments"
FT	FT	Region	189..204 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	190..191 /note="Inter-sub-domain loop"
FT	FT	Cleavage-site	202..203 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	228..229 /note="Break-point between alpha and omega fragments"
FT	FT	Cleavage-site	228..229 /note="Break-point between alpha and omega fragments"
PD	XX	WO200151629-A2.	
PD	XX	19-JUL-2001.	
PD	XX	16-JAN-2001; 2001WO-US001651.	
PD	XX	13-JAN-2000; 2000US-0175968P.	
PD	XX	15-MAR-2000; 2000US-00526106.	

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI; 2001-451857/48.
DR

XX N-PSDB; AAD10411.
DR

XX Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.

XX Claim 38; Fig 2; 104pp; English.
PS

XX The invention relates to new interaction-dependent enzyme association
CC (IdRA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of *Escherichia coli*. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The IdRA systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is *Escherichia coli*
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu
CC
XX

XX Sequence 263 AA;
SQ

Query Match 100.0%; Score 925; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVMADQAGARVGYIELDLSGKILSFPERPERPMMSTFKVLLCGAVLSRID 60

DB 1 HPEITLVKVMADQAGARVGYIELDLSGKILSFPERPERPMMSTFKVLLCGAVLSRID 60

QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAAILLTTIGGP 120

DB 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAAILLTTIGGP 120

QY 121 KETLAFINMGDHYRLDRWPEBELNEALPNDERDITTMVAATTLRKLLTGELLTLASRQ 180

DB 121 KETLAFINMGDHYRLDRWPEBELNEALPNDERDITTMVAATTLRKLLTGELLTLASRQ 180

QY 181 Q 181

DB 181 Q 181

RESULT 2
AAB36692
ID AAB36692 standard; protein; 263 AA.
XX

XX AAB36692;
AC

XX 15-MAR-2001 (first entry)
DT

XX *Escherichia coli* mature TEM-1 beta-lactamase protein sequence.
DE

XX Interaction-activated protein; beta-lactamase; protein interaction.
KM

XX *Escherichia coli*.
OS

XX WO200071702-A1.
PN

XX 30-NOV-2000.
PD

XX 16-MAR-2000; 2000WO-US007108.
PF

XX 25-MAY-1999; 99US-0135926P.
PR

XX 13-JAN-2000; 2000US-0175968P.
PR

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI; 2001-032034/04.
DR

XX N-PSDB; AAC90773.
DR

PT Novel fragment complementation system to identify interactions between
PT polypeptides comprises fragment pairs having first and second members
PT that reassemble into a marker protein which has a directly detectable
PT signal.

PS Disclosure; Fig 2; 94pp; English.
PS

XX The present invention describes a fragment complementation system (I)
XX which comprises a first oligopeptide (OP1) containing an N-terminal
XX fragment with a C-terminal break point and a second oligopeptide (OP2)
XX comprising a C-terminal with a N-terminal breakpoint, in which the C and
XX N terminal fragments are both derived from a marker protein (MP) and
XX reassemble to form a functionally reconstituted MP. Methods from the
XX present invention are used for monitoring the occurrence of protein-
XX protein interactions in a sample, identifying oligopeptide interactions
XX between two different proteomes, identifying epitopes that bind to an
XX immunoglobulin (Ig) variable region, for identifying interactions between
XX an extracellular domain of a transmembrane protein and a polypeptide, for
XX high-throughput identification of compounds that inhibit phosphorylation-
XX regulated signal transducers, forming a enzyme complementation system for
XX selecting simultaneous incorporation of multiple genetic elements into a
XX host cell and for activating a beta-lactam derivative of an antitumor
XX compound in a host who is in need of it. The present sequence represents
XX the *Escherichia coli* mature TEM-1 beta-lactamase, which is used in the
XX exemplification of the present invention
CC

SQ Sequence 263 AA;
SQ

Query Match 100.0%; Score 925; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVMADQAGARVGYIELDLSGKILSFPERPERPMMSTFKVLLCGAVLSRID 60

DB 1 HPEITLVKVMADQAGARVGYIELDLSGKILSFPERPERPMMSTFKVLLCGAVLSRID 60

QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAAILLTTIGGP 120

DB 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGTVRELCSAAITMSDNTAAILLTTIGGP 120

QY 121 KETLAFINMGDHYRLDRWPEBELNEALPNDERDITTMVAATTLRKLLTGELLTLASRQ 180

DB 121 KETLAFINMGDHYRLDRWPEBELNEALPNDERDITTMVAATTLRKLLTGELLTLASRQ 180

QY 181 Q 181
181 Q 181

RESULT 3
ADJ67709

ID ADJ67709 standard; protein; 263 AA.

XX ADJ67709;

XX 20-MAY-2004 (first entry)

DE Escherichia coli TBM-1 beta-lactamase.

XX fragment complementation system; marker protein;

KW multiple genetic element incorporation; antibiotic resistance;

KW beta-lactam derivative activation; anti-tumour compound;

KW functional reassembly; protein-protein interaction; proteome interaction;

KW immunoglobulin variable region; immune cell protein; CD40;

KW phosphorylation-regulated cell signal transducer; TBM-1 beta-lactamase;

KW enzyme.

XX Escherichia coli.

PN US2004038317-A1.

XX 26-FEB-2004.

PF 22-SEP-2003; 2003US-00668778.

XX 15-MAR-1999; 99US-0124339P.

PR 25-MAY-1999; 99US-0135926P.

PR 13-JAN-2000; 2000US-0175968P.

PR 15-MAR-2000; 2000US-00526106.

XX (KALO-) KALOBIO INC.

PI Balint RF, Her J;

XX WPI; 2004-203222/19.

DR N-PSDB; ADJ67708.

PT Fragment complementation system for detecting immunoglobulin epitope, has

XX first oligopeptide containing N-terminal fragment with C-terminal break-

XX point, second oligopeptide containing C-terminal fragment with N-terminal

XX break-point.

PS Disclosure; SEQ ID NO 2; 47pp; English.

XX The invention describes a fragment complementation system (I) comprising

XX a first oligopeptide having an N-terminal fragment with a C-terminal

XX break-point, and a second oligopeptide having a C-terminal fragment with

XX a N-terminal break-point, where the N-terminal fragment and the C-

XX terminal fragment each are derived from a marker protein and reassemble

XX to form a functionally reconstituted marker protein. (I) is useful for

XX selecting simultaneous incorporation of multiple genetic elements into a

XX host cell, and activating a beta-lactam derivative of an anti-tumour

XX compound in a host. The method described is useful for identifying a

XX second oligopeptide to which a first oligopeptide binds, involving co-

XX expressing the first and second oligopeptides. Binding of the first

CC efficiently detects multiple interaction between extracellular and
CC intracellular protein with high throughput format. This is the amino acid
CC sequence of antibiotic resistance enzyme TBM-1 beta-lactamase that can be
CC used as a selectable gene in the fragment complementation system of the
CC invention.

XX SQ Sequence 263 AA;

Query Match 100.0%; Score 925; DB 8; Length 263;
Best Local Similarity 100.0%; Pred. No. 2.9e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVDADEDQAGARVGYIELDNLSKILSEFPERFPFMWSTFKYLICGAVLSRID 60
DB 1 HPETLVKVDADEDQAGARVGYIELDNLSKILSEFPERFPFMWSTFKYLICGAVLSRID 60

QY 61 AGQEQLGRRIRHYSQNDLVYSPVTEKHLLTDGWTVRRLCSAATMSDNTANLLITIGSP 120
DB 61 AGQEQLGRRIRHYSQNDLVYSPVTEKHLLTDGWTVRRLCSAATMSDNTANLLITIGSP 120

QY 121 KETLAFIHMGGHVRRLDWPBRLNEAIPNDRDRTTPVAMATTLLKLTGSLTLASRQ 180
DB 121 KETLAFIHMGGHVRRLDWPBRLNEAIPNDRDRTTPVAMATTLLKLTGSLTLASRQ 180

QY 181 Q 181
181 Q 181

RESULT 4
AAW16634
ID AAW16634 standard; protein; 264 AA.

XX AAW16634;

XX 09-AUG-1997 (first entry)

DE Beta-lactamase (including signal peptide).

XX Gene directed enzyme prodng therapy; GDEPT;

XX virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;

XX HIV; inflammation.

XX Escherichia coli.

XX Key Location/Qualifiers
XX Peptide 1..23
XX /label= Sig_peptide

XX MO9719180-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002845.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Ohmstede C;

XX WPI, 1997-298117/27.

XX N-PSDB; AAW16634.

XX Molecular chimera for gene or virus directed enzyme prodng therapy -
XX useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 28; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16634), including the signal peptide,

XX is the expression product of a molecular chimera, designated PCMV-BL
XX (AAW16637), in which the beta-lactamase gene is under control of the CMV
XX intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodng therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodng into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 925; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGIETDLSNGKILESFRPERFPMSTFKVLCGAVLSRID 60

DB 2 HPEITLVKVDADQAGARVGIETDLSNGKILESFRPERFPMSTFKVLCGAVLSRID 61

QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGCP 120

DB 62 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGCP 121

QY 121 KELTSFLHMGDHTRLDRWPELNEAI PNDERDTTVPVAAATTIRKLLTGELTLASRQ 180

DB 122 KELTSFLHMGDHTRLDRWPELNEAI PNDERDTTVPVAAATTIRKLLTGELTLASRQ 181

QY 181 Q 181

DB 182 Q 182

RESULT 5

AAW18680

ID AAW18680 standard; protein; 264 AA.

AC AAW18680;

DT 13-AUG-1997 (first entry)

DE Intracellularly-expressed beta-lactamase.

KM Prodng therapy; gene directed enzyme prodng therapy; GDEPT;

KW virus directed enzyme prodng therapy; VDEPT; lung cancer;

KM beta-lactamase; PCMV-delBL.

OS Escherichia coli.

PN W09719183-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002846.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAX) GLAXO GROUP LTD.

PI Dev I, Moore JT, Sethna PB;

PT WPI; 1997-298118/27.

DR N-PSDB; AAT70311.

PT DNA construct for gene-directed enzyme prodng therapy of lung cancer -

PT comprises lung- or neuroendocrine-specific promoter controlling

PT expression of prodng-converting enzyme.

PS Example 8iii; Page 32-34; 53pp; English.

XX The intracellular form (AAW18680) of TEM beta-lactamase is expressed by
 CC PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
 CC sequence, minus the signal sequence, is placed under control of the
 CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
 CC lactamase constructs, placed under control of promoter/enhancer elements
 CC of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in prodng therapy of lung

XX cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 925; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 2.9e-94;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGIETDLSNGKILESFRPERFPMSTFKVLCGAVLSRID 60

DB 2 HPEITLVKVDADQAGARVGIETDLSNGKILESFRPERFPMSTFKVLCGAVLSRID 61

QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGCP 120

DB 62 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGCP 121

QY 121 KELTSFLHMGDHTRLDRWPELNEAI PNDERDTTVPVAAATTIRKLLTGELTLASRQ 180

DB 122 KELTSFLHMGDHTRLDRWPELNEAI PNDERDTTVPVAAATTIRKLLTGELTLASRQ 181

QY 181 Q 181

DB 182 Q 182

RESULT 6

AAR31575

ID AAR31575 standard; protein; 286 AA.

AC AAR31575;

DT 10-MAR-2003 (revised)

DT 04-JUN-1993 (first entry)

DE Ampicillin resistance protein.

KM CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

KW xenobiotics; circular; chimeric cytochrome P450IA1.

OS Homo sapiens.

PN US5180666-A.

PD 19-JAN-1993.

PF 27-JUN-1991; 91US-00721775.

PR 27-JUN-1991; 91US-00721775.

PA (UYWA-) UNIV WAYNE STATE.

PI States JC, Hines RN, Novak RF;

PT WPI; 1993-052845/06.

DR N-PSDB; AAQ36498.

PT In vitro method for testing mutagenicity of a chemical - by metabolising

PT chemical cell line consisting of transformed fibroblasts having

PT detectable cytochrome P450 mixed function oxidase activity and detecting

PT gene damage.

PS Disclosure; Col 21-24; 24pp; English.

XX The expression constructs PRNH127 and PRNH155 contain identical sequences
 CC but were constructed using different strategies (see AAQ36498). The
 CC constructs comprise exons 2-7 of human CYP1A1 gene under the control of
 CC the inducible mouse metallothionein (MWT-1) promoter. The constructs also
 CC contain an open reading frame in the opposite orientation to the
 CC cytochrome P450 exons. This ORF encodes ampicillin resistance. The
 CC constructs are suitable for transformation of human fibroblasts derived
 CC from the xeroderma pigmentosum group A. Cultures of the transformed
 CC fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
CC field.)
XX

SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKYLCCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKYLCCGAVLSRID 83
QY 61 ACQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 ACQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITMPVAMATTLRKLTGSELLTLASRQ 180
DB 144 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITMPVAMATTLRKLTGSELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 7

AAR97619
ID AAR97619 standard; protein; 286 AA.

AC AAR97619;

DT 20-AUG-1996 (first entry)

DE Secretary beta-lactamase.

KM Gene therapy; gene directed enzyme prodng therapy; GDEPT;
KM virus directed enzyme prodng therapy; VDEPT; prodng activation;
KM cytotoxic; cytosolic; cancer; tumour; retrovirus; vector;
KM beta-lactamase; cephalosporin.

OS Synthetic.

PN W09616179-A1.

PD 30-MAY-1996.

PF 20-NOV-1995; 95WO-GB002716.

PR 18-NOV-1994; 94GB-00023367.

PA (WELL) WELLCOME FOUND LTD.

PI Dev IK, Moore JT, Ohmerede C;

DR WPI; 1996-268615/27.

DR N-PSDB; AAT9220.

PT Molecular chimera for use in enzyme gene therapy - is activated in a
PT target cell to express a secretable enzyme which cleaves a prodng
PT outside the cell into a cytotoxic or cytostatic agent.

PS Example 3; Page 57-58; 73pp; English.

XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct
XX PCMV-BL (AAT9220), in which the beta-lactamase coding sequence is under
XX the control of the intermediate/early cytomagalovirus promoter. Beta-
XX lacamase delivery to mammalian cells confers sensitivity to
XX cephalosporin prodngs. Liposomal DNA/5-fluorouracil prodng combinations
XX resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival
XX of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
XX was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKYLCCGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDINSKILSFPRPERFPMSTFKYLCCGAVLSRID 83
QY 61 ACQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 ACQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITMPVAMATTLRKLTGSELLTLASRQ 180
DB 144 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITMPVAMATTLRKLTGSELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 8

AAR96423
ID AAR96423 standard; protein; 286 AA.

AC AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

DE Cytochrome P450 (CYP1A1 construct).

KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KM metabolism.

OS Homo sapiens.

PN US5525482-A.

PD 11-JUN-1996.

PF 15-NOV-1994; 94US-00339658.

PR 27-JUN-1991; 91US-00721775.

PR 09-DEC-1992; 92US-00990295.

PA (UTWA-) UNIT WAYNE STATE.

PI Hines RN, Novak RF, States JC;

DR WPI; 1996-286397/29.

DR N-PSDB; AAT30354.

PT Testing chemicals for cytotoxicity to human by detecting gene damage -
PT using recombinant fibroblasts transformed with cytochrome P450 gene under
PT control of inducible promoter.

PS Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-
XX cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNH127 and
XX pRNH15, were isolated by different methods and which both had the same
XX sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
XX of humans to a chemical. The method comprises exposing human fibroblast
XX cells normally not including any cytochrome P450 activity to potentially
XX toxic chemicals. The cells having been transformed to express cytochrome
XX P450, under the control of a controllable promoter through the CYP1A1
XX gene, upon exposure to the chemical in vitro. The chemical is metabolised
XX intracellularly into a cytochrome metabolite by oxidation within the

CC fibroblasts through the intracellular cytochrome P450 mixed function
CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
CC -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAADQAGARVGYIELDLSNGKILSFREPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAADQAGARVGYIELDLSNGKILSFREPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGVTRELCSAATWSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGVTRELCSAATWSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRMEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRMEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 9

AAW16635
ID AAW16635 standard; protein; 286 AA.

XX AAW16635;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (no signal peptide).

XX Gene directed enzyme prodnug therapy; GDEPT;
XX virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;
XX HIV; inflammation.

XX Escherichia coli.

PN WO9719180-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002845.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAX) GLAXO GROUP LTD.

PI Dev I, Moore JT, Ohmstede C;

DR WPI: 1997-298117/27.

DR N-PSDB; AAT66737.

PT Molecular chimera for gene or virus directed enzyme prodnug therapy -
PT useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 26; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
XX is the expression product of a molecular chimera, designated PCMV-delbL
XX (AAT66738), in which the beta-lactamase gene is under control of the CMV
XX intermediate/early promoter. Vectors consisting of a transcriptional
XX regulatory DNA sequence linked to a beta-lactamase gene can be used for
XX enzyme prodnug therapy. Intracellular expression of the beta-lactamase in
XX a targeted cell allows conversion of a prodnug into an agent toxic to
XX the cell for treatment of cancer, viral (e.g. HIV) infection or
XX inflammation

XX Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVAADQAGARVGYIELDLSNGKILSFREPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVAADQAGARVGYIELDLSNGKILSFREPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGVTRELCSAATWSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGVTRELCSAATWSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRMEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRMEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 10

AAW18679
ID AAW18679 standard; protein; 286 AA.

XX AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodnug therapy; gene directed enzyme prodnug therapy; GDEPT;
XX virus directed enzyme prodnug therapy; VDEPT; lung cancer;
XX beta-lactamase; PCMV-BL.

XX Escherichia coli.

PH Key Location/Qualifiers

FT Peptide 1..23

FT Protein /label= Sig_peptide

FT Protein /label= 24..286

FT Protein /label= Mat_protein

PN WO9719183-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002846.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAX) GLAXO GROUP LTD.

PI Dev I, Moore JT, Sethna PB;

DR WPI: 1997-298118/27.

DR N-PSDB; AAT70309.

PT DNA construct for gene-directed enzyme prodnug therapy of lung cancer -
PT comprises lung- or neuroendocrine-specific promoter controlling
PT expression of prodnug-converting enzyme.

XX Example 81; Page 26-27; 53pp; English.

XX The secreted form (AAW18679) of TBM beta-lactamase is expressed by PCMV-
XX BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
XX placed under control of the intermediate/early promoter of
XX cytomegalovirus. Secretory beta-lactamase constructs, placed under
XX control of promoter/enhancer elements of lung-associated protein or
XX neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodrg therapy of lung cancer
XX Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGVGYIELDNLGSKILSPRPFRPMMSTFKYLGGAVLSRID 60
DB 24 HPEITLVKVDADQAGVGYIELDNLGSKILSPRPFRPMMSTFKYLGGAVLSRID 83
QY 61 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 11

AA08529
ID AA08529 standard; protein; 286 AA.

XX AA08529;

DT 03-AUG-1999 (first entry)

DE Vector pASK75 beta-1a protein.

XX Firefly luciferase; tetracycline; transcriptional control; Tetr; TetA;
KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
KM insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
KW allergy.

XX Synthetic.

XX MO9925866-A1.

PD 27-MAY-1999.

XX 11-NOV-1998; 98WO-FI000873.

XX 14-NOV-1997; 97FI-00004235.

XX (KORP/) Korpela M.

PA (KARP/) Karp M.

PA (KURI/) Kurittu J.

PI Korpela M, Karp M, Kurittu J;

XX WPI; 1999-338015/28.

DR N-PSDB; AA072418.

XX Assaying for tetracycline using recombinant prokaryotic cells.

XX Disclosure; Page 47-48; 67pp; English.

XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline from other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxCDABE
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (TetA)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample.

CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected

XX Sequence 286 AA;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGVGYIELDNLGSKILSPRPFRPMMSTFKYLGGAVLSRID 60
DB 24 HPEITLVKVDADQAGVGYIELDNLGSKILSPRPFRPMMSTFKYLGGAVLSRID 83
QY 61 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEOIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDPTTVPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 12

AAB10442
ID AAB10442 standard; protein; 286 AA.

XX AAB10442;

AC 01-DEC-2000 (first entry)

DE Expression vector pSEX15G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

XX Synthetic.

XX DEL9900635-A1.

PD 13-JUL-2000.

XX 11-JAN-1999; 99DE-01000635.

XX 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.

PI Breiting F, Poustka A, Moldenhauer G;

XX WPI; 2000-499832/45.

DR N-PSDB; AAA71430.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 3; 22pp; German.

XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The

invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD53. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the bla protein contained in the expression vector pSEX11G2 which contains the bla protein, Neo-R and protein G described in the method of the invention

SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVAADQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVAADQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 143
QY 121 KETLAFINMGDHTRLDRWEPELNEAIPNDRDTMPVAAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFINMGDHTRLDRWEPELNEAIPNDRDTMPVAAATTLRKLLTSELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 13

AAB10438

ID AAB10438 standard; protein; 286 AA.

AC AAB10438;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11L4 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71428.

Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with antibody library.

Claim 16; Fig 1; 22pp; German.

This invention describes a novel method for the selection of monoclonal antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD53. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the Neo-R protein contained in the expression vector pSEX11L4 which contains the bla protein, Neo-R and protein G described in the method of the invention

SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVAADQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVAADQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGSP 143
QY 121 KETLAFINMGDHTRLDRWEPELNEAIPNDRDTMPVAAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFINMGDHTRLDRWEPELNEAIPNDRDTMPVAAATTLRKLLTSELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 14

AAB10440

ID AAB10440 standard; protein; 286 AA.

AC AAB10440;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71429.

Selecting monoclonal antibodies, by expressing them on the surface of

PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(R)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEK11G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLCGAVLSRID 60
DB 24 HPELVKVDADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLCGAVLSRID 83
QY 61 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITTPVAMATTLLKLTGELTLTASRQ 180
DB 144 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITTPVAMATTLLKLTGELTLTASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 15

AAB50898
ID AAB50898 standard; protein; 286 AA.

AC AAB50898;

DT 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

KM bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KW glucanase; integration vector; pLO12306.

OS Unidentified.

PN WO200071729-A2.

PD 30-NOV-2000.

PF 26-MAY-2000; 2000MO-US014773.

PR 26-MAY-1999; 99US-0136376P.

PA (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;
XX
DR MPI; 2001-032043/04.
DR N-PSDB; AAC91455.

XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PS polysaccharase under control of surrogate promoter.

PS Disclosure; Page 82-83; 87pp; English.

XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC *chrysanthemi*, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence

SQ Sequence 286 AA;

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 3.3e-94;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLCGAVLSRID 60
DB 24 HPELVKVDADBDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLCGAVLSRID 83
QY 61 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 120
DB 84 ACOEQLGRRIHYSQNDLVEYSPVTEKHLDGKMTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITTPVAMATTLLKLTGELTLTASRQ 180
DB 144 KELTAFIHNMGDHYRLDRWPELNEAIPNDRDITTPVAMATTLLKLTGELTLTASRQ 203
QY 181 Q 181
DB 204 Q 204

Search completed: June 10, 2005, 10:49:10
Job time : 71.1783 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 / Search time 18.5574 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925

Sequence: 1 HPELVKVKVADMDQGARVG.....ATTLRKLTGELLTLASRQ 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	925	100.0	286 1 US-07-721-775A-2	Sequence 2, Appl
2	925	100.0	286 1 US-08-339-658-2	Sequence 2, Appl
3	925	100.0	286 3 US-09-263-933-7	Sequence 7, Appl
4	925	100.0	286 3 US-09-263-933-14	Sequence 14, Appl
5	925	100.0	286 3 US-09-263-933-21	Sequence 21, Appl
6	925	100.0	286 3 US-09-025-769B-265	Sequence 265, App
7	925	100.0	286 4 US-09-025-769B-362	Sequence 362, App
8	925	100.0	286 4 US-09-919-901-7	Sequence 7, Appl
9	925	100.0	286 4 US-09-919-901-14	Sequence 14, Appl
10	925	100.0	286 4 US-09-919-901-21	Sequence 21, Appl
11	925	100.0	286 4 US-09-490-070A-265	Sequence 265, App
12	925	100.0	286 4 US-09-490-070A-362	Sequence 362, App
13	925	100.0	286 4 US-09-490-153-265	Sequence 265, App
14	925	100.0	286 4 US-09-490-153-362	Sequence 362, App
15	925	100.0	286 4 US-10-191-966-7	Sequence 7, Appl
16	925	100.0	286 4 US-10-191-966-14	Sequence 14, Appl
17	925	100.0	286 4 US-10-191-966-21	Sequence 21, Appl
18	925	100.0	286 4 US-09-490-324-265	Sequence 265, App
19	925	100.0	286 4 US-09-490-324-362	Sequence 362, App
20	925	100.0	286 4 US-09-025-769B-285	Sequence 285, App
21	925	100.0	286 3 US-09-025-769B-298	Sequence 298, App
22	925	100.0	286 3 US-09-025-769B-300	Sequence 300, App
23	925	100.0	286 4 US-09-490-070A-285	Sequence 285, App
24	925	100.0	286 4 US-09-490-070A-298	Sequence 298, App
25	925	100.0	286 4 US-09-490-070A-300	Sequence 300, App
26	925	100.0	286 4 US-09-490-153-285	Sequence 285, App
27	925	100.0	286 4 US-09-490-153-298	Sequence 298, App

28	925	100.0	299 4 US-09-490-153-300	Sequence 300, App
29	925	100.0	299 4 US-09-490-324-285	Sequence 285, App
30	925	100.0	299 4 US-09-490-324-298	Sequence 298, App
31	925	100.0	299 4 US-09-490-324-300	Sequence 300, App
32	925	100.0	2307 3 US-09-263-933-2	Sequence 2, Appl
33	925	100.0	2307 3 US-09-263-933-9	Sequence 9, Appl
34	925	100.0	2307 3 US-09-263-933-16	Sequence 16, Appl
35	925	100.0	2307 4 US-09-919-901-2	Sequence 2, Appl
36	925	100.0	2307 4 US-09-919-901-16	Sequence 16, Appl
37	925	100.0	2307 4 US-09-919-901-21	Sequence 21, Appl
38	925	100.0	2307 4 US-10-191-966-2	Sequence 2, Appl
39	925	100.0	2307 4 US-10-191-966-9	Sequence 9, Appl
40	925	100.0	2307 4 US-10-191-966-16	Sequence 16, Appl
41	924	99.9	286 4 US-09-555-510B-9	Sequence 9, Appl
42	924	99.9	286 4 US-10-231-013-9	Sequence 9, Appl
43	924	99.9	1293 4 US-09-170-496D-292	Sequence 292, App
44	924	99.9	1293 4 US-09-364-425B-57	Sequence 57, Appl
45	920	99.5	263 1 US-08-407-544-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:

APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

APPLICANT: No. 5180666ak, Raymond F.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING

TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSER: Relating, Echington, Barnard, Perry & Milton

STREET: P. O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07721,775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-721-775A-2

Query Match 100.0%; Score 925; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 4,1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKVADMDQGARVGITLDLNSGKILSFRPEPRPMSFTFYLLCGAVLSRID 60
DB 24 HPELVKVKVADMDQGARVGITLDLNSGKILSFRPEPRPMSFTFYLLCGAVLSRID 83

QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLLHNMGDHVTRLDRWEPLEINBAIPNDRDPTTVPVAAATTIRKLLTGELLTLASRQ 180
DB 144 KELTSFLLHNMGDHVTRLDRWEPLEINBAIPNDRDPTTVPVAAATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 2

US-08-339-658-2
Sequence 2, Application US/08339658
Patent No. 5525482
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Relisting, Echtington, Barnard, Perry & Milton
STREET: P. O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,658
FILING DATE: 15-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,295
FILING DATE: 09-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-658-2

Query Match 100.0%; Score 925; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITVKYKADBDQAGRVGYIELDLSKILSFRRPERFPMSTFKYLLCGAVLSRID 60
DB 24 HPEITVKYKADBDQAGRVGYIELDLSKILSFRRPERFPMSTFKYLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLLHNMGDHVTRLDRWEPLEINBAIPNDRDPTTVPVAAATTIRKLLTGELLTLASRQ 180
DB 144 KELTSFLLHNMGDHVTRLDRWEPLEINBAIPNDRDPTTVPVAAATTIRKLLTGELLTLASRQ 203

QY 181 Q 181
DB 204 Q 204

RESULT 3

US-09-263-933-7
Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKYKADBDQAGRVGYIELDLSKILSFRRPERFPMSTFKYLLCGAVLSRID 60
DB 24 HPEITVKYKADBDQAGRVGYIELDLSKILSFRRPERFPMSTFKYLLCGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTSFLLHNMGDHVTRLDRWEPLEINBAIPNDRDPTTVPVAAATTIRKLLTGELLTLASRQ 180
DB 144 KELTSFLLHNMGDHVTRLDRWEPLEINBAIPNDRDPTTVPVAAATTIRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 4

US-09-263-933-14
Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDLSGKILSPRPFRPMMSTFKVLGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYIELDLSGKILSPRPFRPMMSTFKVLGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTFLHMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTFLHMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 5

US-09-263-933-21
Sequence 21, Application US/09263933

Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDLSGKILSPRPFRPMMSTFKVLGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYIELDLSGKILSPRPFRPMMSTFKVLGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTFLHMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTFLHMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 6

US-09-025-7698-265
Sequence 265, Application US/09025769B

Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-025-7698-265
MOLUCULE TYPE: protein

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDLSGKILSPRPFRPMMSTFKVLGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYIELDLSGKILSPRPFRPMMSTFKVLGAVLSRID 83
QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGNTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTFLHMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTFLHMGDHTRLDRWPELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 7

US-09-025-7698-362
Sequence 362, Application US/09025769B

Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 925; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKAEDQAGAVGYIELDLSGKILSPRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGAVGYIELDLSGKILSPRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KETAFILNMGDHYTRLDRWEPELNEALPNDERDTTVPVAAATTLRKLLTGSELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPELNEALPNDERDTTVPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204
RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGAVGYIELDLSGKILSPRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGAVGYIELDLSGKILSPRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KETAFILNMGDHYTRLDRWEPELNEALPNDERDTTVPVAAATTLRKLLTGSELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPELNEALPNDERDTTVPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQAGAVGYIELDLSGKILSPRPFRPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQAGAVGYIELDLSGKILSPRPFRPMMSTFVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGSP 143
QY 121 KETAFILNMGDHYTRLDRWEPELNEALPNDERDTTVPVAAATTLRKLLTGSELLTLASRQ 180
DB 144 KETAFILNMGDHYTRLDRWEPELNEALPNDERDTTVPVAAATTLRKLLTGSELLTLASRQ 203
QY 181 Q 181

DB 204 Q 204

RESULT 10

US-09-919-901-21

Sequence 21, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:

APPLICANT: Bette, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

US-09-919-901-21

Query Match 100.0%; Score 925; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 4,1e-100; Mismatches 0; Indels 0; Gaps 0;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HPELVKVKADADQAGRVGYIELDLSGKILSPRPERFPMSTFKVLCGAVLSRID 60
DB 24 HPELVKVKADADQAGRVGYIELDLSGKILSPRPERFPMSTFKVLCGAVLSRID 83
QY 61 AGQEQGLRRIRHSQNDLVESVPTKHLTDGTVRELCSAATMSDNTANILTTIGSP 120
DB 84 AGQEQGLRRIRHSQNDLVESVPTKHLTDGTVRELCSAATMSDNTANILTTIGSP 143
QY 121 KETLAFIHMGGHVRILDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ 180
DB 144 KETLAFIHMGGHVRILDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ 203
QY 181 Q 181
DB 204 Q 204
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RESULT 11

US-09-490-070A-265

Sequence 265, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & Mcauliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 100.0%; Score 925; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 4,1e-100; Mismatches 0; Indels 0; Gaps 0;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HPELVKVKADADQAGRVGYIELDLSGKILSPRPERFPMSTFKVLCGAVLSRID 60
DB 24 HPELVKVKADADQAGRVGYIELDLSGKILSPRPERFPMSTFKVLCGAVLSRID 83
QY 61 AGQEQGLRRIRHSQNDLVESVPTKHLTDGTVRELCSAATMSDNTANILTTIGSP 120
DB 84 AGQEQGLRRIRHSQNDLVESVPTKHLTDGTVRELCSAATMSDNTANILTTIGSP 143
QY 121 KETLAFIHMGGHVRILDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ 180
DB 144 KETLAFIHMGGHVRILDRWPELNEAIPNDRDITMPVAMATTIRKLTGELLTASRQ 203
QY 181 Q 181
DB 204 Q 204
```

RESULT 12

US-09-490-070A-362

Sequence 362, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman

White & Mcauliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4,1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQSLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDNTAAILTTTIGP 120
DB 84 AGQSLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDNTAAILTTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4,1e-100; Indels 0; Gaps 0;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGTYIEDLNSGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQSLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDNTAAILTTTIGP 120
DB 84 AGQSLGRRIHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDNTAAILTTTIGP 143
QY 121 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFILNMGDHYTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Reg.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDGARVGYIELDNSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQDGARVGYIELDNSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFLNMGDVTRLDRWPELNEAIPNDERDITMPVAMATTIRKLLTGELITLASRQ 180
DB 144 KETLAFLNMGDVTRLDRWPELNEAIPNDERDITMPVAMATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 925; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDGARVGYIELDNSGKILSPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKVDADQDGARVGYIELDNSGKILSPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 120

DB 84 AGQEQIGRRIRHYSQNDLVESPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFLNMGDVTRLDRWPELNEAIPNDERDITMPVAMATTIRKLLTGELITLASRQ 180
DB 144 KETLAFLNMGDVTRLDRWPELNEAIPNDERDITMPVAMATTIRKLLTGELITLASRQ 203
QY 181 Q 181
DB 204 Q 204

Search completed: June 10, 2005, 11:01:14
Job time : 19.5574 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 13.1993 Seconds
(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181

Perfect score: 925
Sequence: 1 HPETLVKVKDAEDQLGARVQ.....ATTLRKLLTGELTLASRQ 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	286	2 TS1301	beta-lactamase (EC
2	925	100.0	286	2 S47061	beta-lactamase (EC
3	925	100.0	286	4 S41975	beta-lactamase (EC
4	920	99.5	286	1 PNECP	beta-lactamase (EC
5	920	99.5	286	4 I40905	beta-lactamase (EC
6	912	98.6	286	2 S30113	beta-lactamase (EC
7	907	98.1	286	2 S60312	extended spectrum
8	906	97.9	286	2 S60310	extended spectrum
9	906	97.9	286	2 S60311	beta-lactamase (EC
10	906	97.9	286	2 J01546	Bla protein - SalM
11	640	69.2	286	2 S16146	beta-lactamase (EC
12	640	69.2	286	2 A60679	beta-lactamase (EC
13	636	68.8	286	2 S00464	beta-lactamase (EC
14	636	68.8	265	2 S02434	beta-lactamase (EC
15	636	68.8	265	1 A44998	beta-lactamase (EC
16	636	68.8	286	2 A60632	beta-lactamase (EC
17	633	68.4	265	2 A60448	beta-lactamase (EC
18	633	68.4	286	2 A37200	beta-lactamase (EC
19	618	66.8	279	2 A24469	beta-lactamase (EC
20	611.5	66.1	287	1 A44996	beta-lactamase (EC
21	585	63.2	286	1 A44958	beta-lactamase (EC
22	506	54.7	286	2 A41381	beta-lactamase (EC
23	410.5	44.4	281	2 D95395	probable beta lact
24	395.5	42.8	314	2 S06967	beta-lactamase (EC
25	392.5	42.4	294	2 S16553	beta-lactamase (EC
26	386	41.7	293	3 S04649	beta-lactamase (EC
27	383.5	41.5	306	1 S45822	beta-lactamase (EC
28	382.5	41.4	302	2 S36188	beta-lactamase (EC
29	380.5	41.1	263	2 A54543	beta-lactamase (EC

30	377.5	40.8	291	2 S42075	beta-lactamase (EC
31	372.5	40.3	306	2 G69674	beta-lactamase (EC
32	371.5	40.2	311	2 JN0520	beta-lactamase (EC
33	368	39.8	305	2 A61156	beta-lactamase (EC
34	368	39.8	305	2 A57002	beta-lactamase (EC
35	368	39.8	305	2 A60680	beta-lactamase (EC
36	367.5	39.7	306	2 S47330	penicillinase - Ba
37	359.5	38.9	291	2 JP0074	beta-lactamase (EC
38	357	38.6	310	2 J10091	beta-lactamase (EC
39	356.5	38.5	305	1 C45822	beta-lactamase (EC
40	354.5	38.3	263	2 S23929	beta-lactamase (EC
41	354.5	38.3	288	2 UQ1136	beta-lactamase (EC
42	354	38.3	294	2 S04080	beta-lactamase (EC
43	353.5	38.2	311	1 S02714	beta-lactamase (EC
44	350.5	37.9	304	2 A49789	beta-lactamase (EC
45	350.5	37.9	304	2 A35001	beta-lactamase (EC

ALIGNMENTS

RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: TS1301
R:WACH, A.; BRACHAT, A.; ALBERTISSEGUI, C.; REISCHUNG, C.; PHILIPSEN, P.
Yeast 13, 1065-1075, 1997
A:Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A:Reference number: Z09587
A:Accession: TS1301
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <MAC>
A:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
A:Genetics:
A:Gene: bla
A:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 100.0%; Score 925; DB 2; Length 286;
Best local similarity 100.0%; Pred. No. 2.5e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPETLVKVKDAEDQLGARVGYIELDNGSKIIESFRPEERFPMSTFKYLICGAVLSRID	60
DB	24	HPETLVKVKDAEDQLGARVGYIELDNGSKIIESFRPEERFPMSTFKYLICGAVLSRID	83
QY	61	AGQEQIGRIHYSQNDIVESPYTEKHLTDGWTVELCSAATIMSDNTAANLLTTIGSP	120
DB	84	AGQEQIGRIHYSQNDIVESPYTEKHLTDGWTVELCSAATIMSDNTAANLLTTIGSP	143
QY	121	KELTAFILNMGDVTRLDRLRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ	180
DB	144	KELTAFILNMGDVTRLDRLRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ	203
QY	181	Q 181	
DB	204	Q 204	

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C:Species: phage phi-X174
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S47061
R:Henrich, B.; Schmidtberger, B.
Submitted to the EMBL Data Library, July 1994
A:Description: A variant of phiX174 gene B-based positive selection vectors with enhanced
A:Reference number: S47060
A:Accession: S47061

A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <HEN>
 A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
 C:Superfamily: beta-lactamase I
 C:Keywords: hydrolase

Query Match 100.0%; Score 925; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.5e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGTEIDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB HPEITLVKVDADQAGRVGTEIDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 120
 DB AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 143
 QY 121 KELTAFILNMGDHTRLDRWEPPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB KELTAFILNMGDHTRLDRWEPPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 3
 S11975
 beta-lactamase (EC 3.5.2.6) precursor - synthetic
 C:Species: synthetic
 C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
 C:Accession: S41975
 R:Kaschner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, G.
 Gene 148, 67-70, 1994
 A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar
 A:Reference number: A57991; MUID:95011660; PMID:7926839
 A:Accession: S41975
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-286 <KAS>
 A:Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623
 A:Note: submitted to the EMBL Data Library, December 1993
 C:Keywords: hydrolase

Query Match 100.0%; Score 925; DB 4; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.5e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGTEIDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB HPEITLVKVDADQAGRVGTEIDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 120
 DB AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 143
 QY 121 KELTAFILNMGDHTRLDRWEPPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB KELTAFILNMGDHTRLDRWEPPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 4
 PNECP
 beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmids
 N:Alternate names: beta-lactamase TEM-6 (for blaT-6 DNA); penicillinase
 C:Species: Escherichia coli
 C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005
 R:Sutcliffe, J.G.
 Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
 A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid
 A:Reference number: A93821; MUID:79012484; PMID:358200
 A:Accession: A93821
 A:Molecule type: DNA
 A:Residues: 1-286 <STU>
 A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:g43710; PIDN:CAA23886.1; P1
 A:Experimental source: plasmid pBR322

R:Ambler, R.P.; Scott, G.K.
 Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
 A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid f
 A:Reference number: A93820; MUID:79012483; PMID:358199
 A:Accession: A93820
 A:Molecule type: protein
 A:Residues: 24-36, 'K', 38-286 <AMB>
 A:Experimental source: plasmid R6K
 R:Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
 J. Bacteriol. 172, 3040-3050, 1990
 A:Title: The kil-kor region of broad-host-range plasmid RK2: nucleotide sequence, polype

A:Reference number: A35387; MUID:90264294; PMID:2160936
 A:Accession: A35387
 A:Molecule type: DNA
 A:Residues: 182-286 <KOR>
 A:Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1; PID:g152522
 A:Experimental source: PK2
 R:Goussard, S.; Sougkoff, W.; Mabilat, C.; Baumenfeind, A.; Courvalin, P.
 U. Gen. Microbiol. 137, 2681-2687, 1991
 A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum

A:Reference number: S24415; MUID:92166702; PMID:1665171
 A:Accession: S24415
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>
 A:Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
 A:Experimental source: ISI-like blaT-6 DNA
 R:Sutcliffe, J.G.
 Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
 A:Reference number: A90923; MUID:80002802; PMID:383387
 A:Contents: annotation
 C:Comment: like most penicillinases from gram-negative bacteria, this enzyme, coded by a
 C:Genetics:
 A:Genome: plasmid
 C:Superfamily: Beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein
 F:1-23/Domains: signal sequence #status predicted <SIG>
 F:24-286/Product: beta-lactamase #status experimental <MAT>
 F:68/Active site: Ser #status predicted
 F:75-121/Diulfide bonds: #status predicted

Query Match 99.5%; Score 920; DB 1; Length 286;
 Best Local Similarity 98.9%; Pred. No. 7.2e-76;
 Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGTEIDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
 DB HPEITLVKVDADQAGRVGTEIDLSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 120
 DB AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANILLTTIGP 143
 QY 121 KELTAFILNMGDHTRLDRWEPPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB KELTAFILNMGDHTRLDRWEPPELNEAIPNDRDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

RESULT 5

140905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A>Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*
C/Date: 15-Aug-1996 #sequence_reviseion 16-Aug-1996 #text_change 20-Oct-2000
C/Accession: 140905
R:Taylor, J.; Stearman, R.S.; Urcanti, B.B.
Plasmid 29, 241-244, 1993
A>Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A/Reference number: 140904; MUID:93361581; PMID:7689234
A/Accession: 140905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RES>
A:Cross-references: EMBL:U21228; NID:9885956; PIDN:AAA70411.1; PID:9885958
C:Keywords: hydrolase

Query Match 99.5%; Score 920; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 7, 2e-76;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 60
Db HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 83
Qy 61 AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 120
Db AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 143
Qy 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLRKLLTGELTLASRQ 180
Db KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLRKLLTGELTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 6

S30113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCF04
C:Species: *Klebsiella pneumoniae*
C/Date: 30-Sep-1993 #sequence_reviseion 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: S30113
R:Mabilat, C.; Lourencao-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A>Title: A new example of physical linkage between *Tn1* and *Tn21*: the antibiotic multiple
A/Reference number: S30112; MUID:93062798; PMID:1331747
A/Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MA>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:943797; PIDN:CAA45828.1; PID:943798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.6%; Score 912; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 3, 8e-75;
Matches 177; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 60
Db HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 83
Qy 61 AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 120
Db AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 143
Qy 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLRKLLTGELTLASRQ 180

Db 144 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLRKLLTGELTLASRQ 203

Qy 181 Q 181
Db 204 Q 204

RESULT 7

S60312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C/Date: 12-Apr-1996 #sequence_reviseion 19-Apr-1996 #text_change 22-Jun-1999
C/Accession: S60312
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A>Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: EMBL:X65254; NID:9296955; PIDN:CAA46346.1; PID:9296956
C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 907; DB 2; Length 286;
Best Local Similarity 97.2%; Pred. No. 1, 1e-74;
Matches 176; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 60
Db HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 83
Qy 61 AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 120
Db AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 143
Qy 121 KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLRKLLTGELTLASRQ 180
Db KELTAFLLNMGDHYTRLDRWPELNEALPNDERDITMPVAAATTLRKLLTGELTLASRQ 203
Qy 181 Q 181
Db 204 Q 204

RESULT 8

S60310
extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C/Date: 12-Apr-1996 #sequence_reviseion 19-Apr-1996 #text_change 22-Jun-1999
C/Accession: S60310
R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A>Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60310
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: EMBL:X65252; NID:9296951; PIDN:CAA46344.1; PID:9296952
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 906; DB 2; Length 286;
Best Local Similarity 97.2%; Pred. No. 1, 3e-74;
Matches 176; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 60
Db HPELVKVKADBDQAGAVGYIELDLSNGKILESFRPERPFWSTFKVLLCGAVLSRD 83
Qy 61 AGOELGRRIRHSQNDLVYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 120

Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60311, F37392, F00498
R:Chanal, C.; Foupert, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
AntiMicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60311
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969
R:Toimasky, M.E.
plasmid 24, 218-226, 1990
A:Title: Sequencing and expression of aadA, bla, and tnpR from the multi-resistance trans
A:Reference number: A57392; MUID:91172904; PMID:1963948
A:Accession: F37392
A:Molecule type: DNA
A:Residues: 1-32 <TOL>
A:Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C:Genetics:
A:Gene: TEM-bla
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 97.9%; Score 906; DB 2; Length 286;
Best Local Similarity 97.2%; Pred. No. 1.3e-74;
Matches 176; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKXDAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 83
QY 61 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 120
Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 10

QJ0156
bla protease - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: U01546
R:Canon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: U01538; MUID:92383313; PMID:1325061
A:Accession: U01546
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q9L2F9
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 906; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 1.3e-74;
Matches 177; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKXDAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKXDAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 83
QY 61 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 120
Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 203
QY 181 Q 181
Db 204 Q 204

RESULT 11

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146; A53395; S18767
R:Podbielski, A.; Schoenling, U.; Melzer, B.; Wernatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A:Experimental source: plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Sivanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A53395; MUID:90264317; PMID:2160941
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LBE>
A:Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A:Experimental source: plasmid BW77
C:Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.2%; Score 640; DB 2; Length 286;
Best Local Similarity 67.8%; Pred. No. 1.7e-50;
Matches 122; Conservative 26; Mismatches 32; Indels 0; Gaps 0;

QY 2 PETLVKXDAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 61
Db 23 PETLVKXDAEDQAGAVGYIEIDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRD 82
QY 62 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 121
Db 83 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGWTVELCSAAITMSDNTAANILLTTIGP 142
QY 122 ELTAFILNMGDHVTRLDRWPELNEALPNDERDITMPVAMATTLRKLLTGELTLASRQ 181

Db 23 PQLPQLSSESLSGRVKMIEMDLASGRITLWPRADRRFPWMTSTFKVVLGAVLARVDA 82
QY 62 GQOLGRRIHYSONDLVRYSPVTEKHLTDGWTVRRLCSAITMSDNTAANLLTTIGPK 121
Db 83 GDEOLERKIHRYQODLVDPVSEKHLADGKTVGELCAAITMSDNSANLHLATVGGPA 142
QY 122 ELTAFLHNMGDHVTRELDREPELENEAIPNDERDTTTPVAMATTLRKLLTGELLTLASROQ 181
Db 143 GLTAFRLQIGDNVTRLDRETELENEALPGDARDTTTPASMAATLRLKLLTSQRLSARSOQ 202

Search completed: June 10, 2005, 10:58:45
Job time : 14.193 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 60.6383 Seconds
 (without alignments)
 1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_181
 Perfect score: 925
 Sequence: 1 HPEITLVKVKYDABDQIGARVG.....ATTIRKLTGTGELLTLASRQ 181

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03: *
 1: uniprot_sprot: *
 2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	925	100.0	229	2	Q6WY5 Klebsiella
2	925	100.0	232	2	Q6WY4 Klebsiella
3	925	100.0	241	2	Q6WY8 Klebsiella
4	925	100.0	242	2	Q6WY3 Klebsiella
5	925	100.0	285	2	Q6KB67 Klebsiella
6	925	100.0	286	2	Q38058 Klebsiella
7	925	100.0	286	2	Q00626 Klebsiella
8	925	100.0	286	2	Q79C16 Klebsiella
9	925	100.0	286	2	Q79D33 Klebsiella
10	925	99.5	225	2	Q38212 Klebsiella
11	920	99.5	232	2	Q6PRU7 Klebsiella
12	920	99.5	255	2	Q84H50 Klebsiella
13	920	99.5	261	2	Q84H49 Klebsiella
14	920	99.5	264	2	Q6PRU6 Klebsiella
15	920	99.5	281	2	Q6QIV0 Klebsiella
16	920	99.5	282	2	Q6QIV1 Klebsiella
17	920	99.5	286	1	BLAT_ECOLI
18	920	99.5	286	1	BLAT_SALTI
19	920	99.5	286	2	Q53043 Klebsiella
20	920	99.5	286	2	Q8KSD3 Klebsiella
21	920	99.5	286	2	Q8VPA3 Klebsiella
22	920	99.5	286	2	Q93328 Klebsiella
23	920	99.5	286	2	Q934D7 Klebsiella
24	920	99.5	286	2	Q934D7 Klebsiella
25	920	99.5	286	2	Q93G13 Klebsiella
26	920	99.5	286	2	Q6A253 Klebsiella
27	920	99.5	286	2	Q6LBN9 Klebsiella
28	920	99.5	286	2	Q6LCV6 Klebsiella
29	920	99.5	286	2	Q6TMM1 Klebsiella
30	920	99.5	286	2	Q6UVM7 Klebsiella
31	920	99.5	286	2	Q6WJ74 Klebsiella

32	920	99.5	286	2	Q6W9J1 Klebsiella
33	920	99.5	286	2	Q6WY2 Klebsiella
34	920	99.5	286	2	Q6WZD4 Klebsiella
35	920	99.5	286	2	Q7B3X5 Klebsiella
36	920	99.5	286	2	Q7B899 Klebsiella
37	920	99.5	286	2	Q7BP57 Klebsiella
38	920	99.5	286	2	Q7BR75 Klebsiella
39	920	99.5	286	2	Q7DFY3 Klebsiella
40	920	99.5	286	2	Q7DHD3 Klebsiella
41	920	99.5	286	2	Q844X1 Klebsiella
42	920	99.5	286	2	Q8GAB5 Klebsiella
43	920	99.5	286	2	Q9EYX1 Klebsiella
44	920	99.5	286	2	Q9K582 Klebsiella
45	920	99.5	286	2	Q9R770 Klebsiella

ALIGNMENTS

RESULT 1	Q6WY5	PRELIMINARY	PRT	229 AA
ID	Q6WY5			
AC	Q6WY5			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
DE	Beta-lactamase (Fragment).			
GN	Name=BLATEM;			
OS	Klebsiella oxytoca.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Klebsiella.			
OX	NCBI_TaxID=571;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MISC126;			
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;			
RL	Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AY265885; AAP93843.1; .			
DR	HSSP; P00897; 1KGE.			
DR	InterPro; IPR000871; Beta_lactamase_A.			
DR	PRINTS; PR00118; BLACTAMASEA.			
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
FT	NON_TER 1			
FT	NON_TER 1			
SQ	SEQUENCE 229 AA; 25067 MW; C85582C2617F4467 CRC64;			
Query Match	100.0%; Score 925; DB 2; Length 229;			
Best Local Similarity	100.0%; Pred. No. 1.7e-71;			
Matches 181; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 HPEITLVKVKYDABDQIGARVGITIEDLNSGKILSFRRPRPPMSTFVYLCAVLSRID 60			
DB	2 HPEITLVKVKYDABDQIGARVGITIEDLNSGKILSFRRPRPPMSTFVYLCAVLSRID 61			
QY	61 AGQEQGRIRHSQNDLVESPVTEKHLTDGWTVEILCSAITSNDPNAANLITTTIGCP 120			
DB	62 AGQEQGRIRHSQNDLVESPVTEKHLTDGWTVEILCSAITSNDPNAANLITTTIGCP 121			
QY	121 KETLAFILNMGDHYRLDRWEPELNEALPNDERDTTMEVAAATTKLTLTGELLTLASRQ 180			
DB	122 KETLAFILNMGDHYRLDRWEPELNEALPNDERDTTMEVAAATTKLTLTGELLTLASRQ 181			
QY	181 Q 181			
DB	182 Q 182			
RESULT 2	Q6WY4	PRELIMINARY	PRT	232 AA
ID	Q6WY4			
AC	Q6WY4			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Haflnia alvei.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Haflnia.
 OX NCBI_TaxID=569;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC198;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY265886; AAP93844.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 232
 SQ SEQUENCE 232 AA; 25380 MW; 3D5DPD88582C261 CRC64;

Query Match 100.0%; Score 925; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 1.7e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 2 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 61
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
 DB 62 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 121
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 180
 DB 122 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 181
 QY 181 Q 181
 DB 182 Q 182

RESULT 3
 O6MWY8 PRELIMINARY; PRT; 241 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Klebsiella pneumoniae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC112;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY265882; AAP93840.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 925; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.8e-71;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 7 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 66
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
 DB 67 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 126
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 180
 DB 127 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 186
 QY 181 Q 181
 DB 187 Q 187

RESULT 4
 O6MWY3 PRELIMINARY; PRT; 242 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY265887; AAP93845.1; -.
 DR HSSP; P00807; 1KGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 242
 SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 925; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 1.8e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 60
 DB 8 HPELVKVKADADQAGAVGYIELDLSGKILSFRRPFRPMMSTFVLLCGAVLSRID 67
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 120
 DB 68 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTIGP 127
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 180
 DB 128 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAAATTLRKLLTSELTLASRQ 187
 QY 181 Q 181
 DB 188 Q 188

RESULT 5
 O6KB67 PRELIMINARY; PRT; 285 AA.
 ID O6KB67
 AC O6KB67;

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Specific leaf.
 RA Jansen C., Korell M., Ekeley C., Biedenkopf D., Kogel K.H.;
 RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ717739; CAG30723.1; -.
 DR HSSP; P00807; 1A0.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Hypothetical protein.
 FT NON_TER 285
 SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;
 Query Match 100.0%; Score 925; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.2e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 143
 QY 121 KELITAFILNMGDHTVRLDRWPELNEALPNDERDTTPVAMATTIRKLLTGELTLASRQ 180
 DB 144 KELITAFILNMGDHTVRLDRWPELNEALPNDERDTTPVAMATTIRKLLTGELTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204
 RESULT 6
 ID Q38058 PRELIMINARY; PRT; 286 AA.
 AC Q38058;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta lactamase.
 GN Name:bla;
 OS Bacteriophage phi-X174.
 OC Viruses; ssDNA viruses; Microviridae; Microvirinae.
 OX NCBI_TaxID=10847;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
 RA Henrich B., Schmitzberger B.;
 RT "A variant of phiX174 gene E-based positive selection vectors with
 RT enhanced lytic potential.";
 RL Gene 154:51-54(1995).
 DR EMBL; Z35638; CAA84692.1; -.
 DR PIR; S47061; S47061.
 DR HSSP; Q9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.

SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 925; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.2e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 143
 QY 121 KELITAFILNMGDHTVRLDRWPELNEALPNDERDTTPVAMATTIRKLLTGELTLASRQ 180
 DB 144 KELITAFILNMGDHTVRLDRWPELNEALPNDERDTTPVAMATTIRKLLTGELTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204
 RESULT 7
 ID Q00626 PRELIMINARY; PRT; 286 AA.
 AC Q00626; O08022; O08102; O09393; O09396; O09397; O09398; O09399;
 AC O09400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
 AC O09408; O09481; O09482; O09483; O09490; Q57339;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Beta-lactamase.
 OS Staphylococcus aureus.
 OG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP PLASMID=J3356/POX7/3, and J3356/POX7/1;
 RC MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
 RA Needham C., Noble W.C., Dyke K.G.;
 RT "The staphylococcal insertion sequence IS257 is active.";
 RL Plasmid 34:198-205(1995).
 DR EMBL; U36912; AAB39957.1; -.
 DR EMBL; U36911; AAB39956.1; -.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Plasmid.
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;
 Query Match 100.0%; Score 925; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 2.2e-71;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HPEITLVKVDADQAGVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKVDADQAGVGYIELDLSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 120
 DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANILLTTIGSP 143
 QY 121 KELITAFILNMGDHTVRLDRWPELNEALPNDERDTTPVAMATTIRKLLTGELTLASRQ 180
 DB 144 KELITAFILNMGDHTVRLDRWPELNEALPNDERDTTPVAMATTIRKLLTGELTLASRQ 203
 QY 181 Q 181
 DB 204 Q 204

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RESULT 8
ID Q79CL6 PRELIMINARY: PRT: 286 AA.
AC Q79CL6:
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Beta-lactamase.
GN Name-bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylotiales;
OC Methylotiales; Methylobacillus.
OX NCBI_TaxID=405;
RN RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Serbrinjski I.G., Vassan V.M., Tsygankov Y.D.;
RT "Two new members of the B108 superfamily: cloning, sequencing and
RT expression of the B108 genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum."
RN Gene 175:15-22(1996).
RL [2]
RP SEQUENCE FROM N.A.
RA Serbrinjski I., Vassan V., Tsygankov Y.D.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U1280; AAC4581.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-71;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVYLICGAVLSRID 83
QY 61 AGQOLGRRIHYSQNDLVEYSPTVEKHLTDGWTREICSAITMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIHYSQNDLVEYSPTVEKHLTDGWTREICSAITMSDNTAANLLTTIGSP 143
QY 121 KeltaFLNMGDHTRLDREPELNEAIPNDRDITMPVANAATTIRKLTGELLTLASRQ 180
DB 144 KeltaFLNMGDHTRLDREPELNEAIPNDRDITMPVANAATTIRKLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

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RC STRAIN-K-12;
RA Manewannakul K., Manewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12; PLASMID=PRP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breilting F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=PCAPS;
RX MEDLINE=98189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the csp gene
RT Escherichia coli."
RL Anal. Biochem. 257:203-209(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey."
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; AJ001614; CAA04868.1; -.
DR EMBL; AY425988; AAQ95605.1; -.
DR HSSP; P00807; IALQ.
DR GO; GO:008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; Plasmid; Signal.
FT SIGNAL 1 23 Potential.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;

Query Match 100.0%; Score 925; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.2e-71;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVYLICGAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIEIDLSGKILSFRRPFRPMMSTFVYLICGAVLSRID 83
QY 61 AGQOLGRRIHYSQNDLVEYSPTVEKHLTDGWTREICSAITMSDNTAANLLTTIGSP 120
DB 84 AGQOLGRRIHYSQNDLVEYSPTVEKHLTDGWTREICSAITMSDNTAANLLTTIGSP 143
QY 121 KeltaFLNMGDHTRLDREPELNEAIPNDRDITMPVANAATTIRKLTGELLTLASRQ 180
DB 144 KeltaFLNMGDHTRLDREPELNEAIPNDRDITMPVANAATTIRKLTGELLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

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RESULT 9
ID Q79DR3 PRELIMINARY: PRT: 286 AA.
AC Q79DR3:
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name-bla; Synonyms=blatEM-116;
OS Escherichia coli.
OG Plasmid pBP4, and plasmid pCAPs.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN RN
RP SEQUENCE FROM N.A.

```

```

RESULT 10
ID Q38212 PRELIMINARY: PRT: 225 AA.
AC Q38212:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Bacteriophage f1-R208 amplicillinase gene mutation. (Fragment).

```

OS Bacteriophage f1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10863;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Badie J.S., Conrad M.;
RT "O-6-methylguanine mutation and repair is nonuniform: selection for
DNA most interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885(1986).
DR EMBL; M14017; AAA32208.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;

Query Match 99.5%; Score 920; DB 2; Length 225;
Best Local Similarity 98.9%; Pred. No. 4.5e-71;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 60
DB 24 HPETLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 83
OY 61 AGQEQLGRRRIHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 84 AGQEQLGRRRIHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 143
OY 121 KELTSFLNMGDHYRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLTASRQ 180
DB 144 KELTSFLNMGDHYRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLTASRQ 203
OY 181 Q 181
DB 204 Q 204

RESULT 11
O6PRU7 PRELIMINARY; PRT; 232 AA.
AC O6PRU7;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U3;
RA Chandil S., Hoesel-Mazinani S.M.;
RL Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583761; AAS86427.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285BE70EB0 CRC64;

Query Match 99.5%; Score 920; DB 2; Length 232;
Best Local Similarity 98.9%; Pred. No. 4.6e-71;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 60
DB 15 HPETLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 74
OY 61 AGQEQLGRRRIHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 75 AGQEQLGRRRIHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 134
OY 121 KELTSFLNMGDHYRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLTASRQ 180
DB 135 KELTSFLNMGDHYRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLTASRQ 194
OY 181 Q 181
DB 195 Q 195

RESULT 12
O84H50 PRELIMINARY; PRT; 255 AA.
ID O84H50
AC O84H50;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Paaou A., Lavestein-Vanhal M.A.;
RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130282; AAN05026.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.5%; Score 920; DB 2; Length 255;
Best Local Similarity 98.9%; Pred. No. 5.2e-71;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HPETLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 60
DB 12 HPETLVKVDADQAGARVGYIELDLSGKILSFPRPERFPMSTFKYLLCGAVLSRID 71
OY 61 AGQEQLGRRRIHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 120
DB 72 AGQEQLGRRRIHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANILLTTIGSP 131
OY 121 KELTSFLNMGDHYRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLTASRQ 180
DB 133 KELTSFLNMGDHYRLDRWPELNEAIPNDRDITMPAAMATTIRKLLTGELTLTASRQ 191
OY 181 Q 181
DB 192 Q 192

RESULT 13
O84H49 PRELIMINARY; PRT; 261 AA.
ID O84H49
AC O84H49;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).

OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN
RP SEQUENCE FROM N.A.
RL Box A.T.A., Pauw A., Leverstein-Vanhal M.A., Verhoef J., Fluit A.C.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; O9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
FT NON TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F773A08CBB CRC64;

Query Match 99.5%; Score 920; DB 2; Length 261;
Best Local Similarity 98.9%; Pred. No. 5.3e-71;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60
DB 12 HPEITLVKVKDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRD 71
QY 61 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 120
DB 72 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 131
QY 121 KELTSALFNMGDHVTLRDWEPELNEALPNDERDTMPVAMATTLRKLLTGBLLTLASRQ 180
DB 132 KELTSALFNMGDHVTLRDWEPELNEALPNDERDTMPVAMATTLRKLLTGBLLTLASRQ 191
QY 181 Q 181
DB 192 Q 192
RESULT 14
Q6PRU6 PRELIMINARY; PRT; 264 AA.
AC Q6PRU6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE TEM beta-lactamase (fragment).
OS Acinetobacter sp. U1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=U1;
RA Chandali S., Hosseini-Mazinan S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583762; AAS6428.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 1
FT NON TER 264
SQ SEQUENCE 264 AA; 28986 MW; AAF071CF7489352C CRC64;

Query Match 99.5%; Score 920; DB 2; Length 264;
Best Local Similarity 98.9%; Pred. No. 5.4e-71;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60

DB 12 HPEITLVKVKDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRD 71
QY 61 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 120
DB 72 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 131
QY 121 KELTSALFNMGDHVTLRDWEPELNEALPNDERDTMPVAMATTLRKLLTGBLLTLASRQ 180
DB 132 KELTSALFNMGDHVTLRDWEPELNEALPNDERDTMPVAMATTLRKLLTGBLLTLASRQ 191
QY 181 Q 181
DB 192 Q 192

RESULT 15
Q6QIV0 PRELIMINARY; PRT; 281 AA.
AC Q6QIV0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (fragment).
GN Name=blatEM-1;
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yacuyuanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY538700; AAS46846.1; -.
DR EMBL; AY538701; AAS46847.1; -.
DR EMBL; AY538702; AAS46848.1; -.
DR EMBL; AY538698; AAS46844.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 281
FT NON TER 30837
SQ SEQUENCE 281 AA; 30837 MW; C6934B9C696057BP CRC64;

Query Match 99.5%; Score 920; DB 2; Length 281;
Best Local Similarity 98.9%; Pred. No. 5.8e-71;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRD 60
DB 24 HPEITLVKVKDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRD 83
QY 61 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANLLTTIGSP 143
QY 121 KELTSALFNMGDHVTLRDWEPELNEALPNDERDTMPVAMATTLRKLLTGBLLTLASRQ 180
DB 144 KELTSALFNMGDHVTLRDWEPELNEALPNDERDTMPVAMATTLRKLLTGBLLTLASRQ 203
QY 181 Q 181
DB 204 Q 204

Search completed: June 10, 2005, 10:57:00
Job time : 61.6383 secs

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI: 2001-451857/48.
DR

XX N-PSDB; AAD10411.
DR

XX Interaction-dependent enzyme association systems for detecting
PT interactions between two or three polypeptides, especially in human
PT therapeutics, diagnostics or prognostics, comprise circularly permuted
PT proteins.

XX Claim 38; Fig 2; 104bp; English.
PS

XX The invention relates to new interaction-dependent enzyme association
CC (IdRA) systems that comprise a fusion sequence that encodes for a
CC circularly permuted, interaction-activated proteins that reassemble to
CC form functionally reconstituted marker proteins which produce a
CC detectable signal upon the association of two oligopeptides, or upon
CC simultaneous association of two oligopeptides with a third oligopeptide.
CC The marker protein is preferably a type A beta-lactamase, especially TEM-
CC 1 beta-lactamase of *Escherichia coli*. The oligopeptide is a member of a
CC proteome library selected from single chain antibody Fv fragment library,
CC an antibody light chain variable region library and a peptide library
CC displayed within thioredoxin. The IdRA systems are useful for detecting
CC and identifying interactions between intracellular as well as
CC extracellular proteins, particularly between two or three polypeptides.
CC The systems are also useful in selecting with a single marker protein the
CC incorporation of multiple genetic traits in a host cell. In particular,
CC the systems are useful in many applications in human therapeutics,
CC diagnostics and prognostics, as well as in high-throughput screening
CC systems for the discovery and validation of pharmaceutical targets and
CC drugs. Prior systems (e.g. B. coli Dimer Detection System, yeast two-
CC hybrid system or Selective Infective Phage System) require multiple steps
CC between interaction and phenotype, which cause severe loss of efficiency
CC due to high false positive and false negative rates. The present system
CC is capable of simultaneous detection of multiple interactions between
CC extra-cellular as well as intracellular proteins in a high throughput
CC format. The circularly permuted marker proteins comprising interaction-
CC dependent enzymes find use in cell-based sensors for activation or
CC inhibition of metabolic or signal transduction pathways, in high-
CC throughput mapping of pair-wise protein-protein interactions within and
CC between the proteomes of cells, tissues and pathogenic organisms, and in
CC cell-based screens for high-throughput selection of inhibitors of any
CC protein-protein interaction. The present sequence is *Escherichia coli*
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
CC lactamase is a product of ampicillin resistance gene. The enzyme has two
CC domains, alpha-omega and mu
XX

XX Sequence 263 AA;
SQ

Query Match 100.0%; Score 975; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 6.6e-98;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFKVLLCGAVLSRID 60
DB 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFKVLLCGAVLSRID 60
QY 61 AGQEQLGRRIRHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGSP 120
DB 61 AGQEQLGRRIRHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGSP 120
QY 121 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
DB 121 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
QY 181 QLIDWMEADK 190
DB 181 QLIDWMEADK 190

RESULT 2
AAB36692
ID AAB36692 standard; protein; 263 AA.

XX AAB36692;
AC

XX 15-MAR-2001 (first entry)
DT

XX *Escherichia coli* mature TEM-1 beta-lactamase protein sequence.
DE

XX Interaction-activated protein; beta-lactamase; protein interaction.
KW

XX *Escherichia coli*.
OS

XX WO200071702-A1.
PN

XX 30-NOV-2000.
PD

XX 16-MAR-2000; 2000WO-US007108.
PF

XX 25-MAY-1999; 99US-0135926P.
PR

XX 13-JAN-2000; 2000US-0175968P.
PR

XX (PANO-) PANORAMA RES INC.
PA

XX Balint RF, Her J;
PI

XX WPI: 2001-032034/04.
DR

XX N-PSDB; AAC90773.
DR

XX Novel fragment complementation system to identify interactions between
PT polypeptides comprises fragment pairs having first and second members
PT that reassemble into a marker protein which has a directly detectable
PT signal.

XX Disclosure; Fig 2; 94bp; English.
PS

XX The present invention describes a fragment complementation system (I)
CC which comprises a first oligopeptide (OP1) containing an N-terminal
CC fragment with a C-terminal break point and a second oligopeptide (OP2)
CC comprising a C-terminal with a N-terminal breakpoint, in which the C and
CC N terminal fragments are both derived from a marker protein (MP) and
CC reassemble to form a functionally reconstituted MP. Methods from the
CC present invention are used for monitoring the occurrence of protein-
CC protein interactions in a sample, identifying oligopeptide interactions
CC between two different proteomes, identifying epitopes that bind to an
CC immunoglobulin (Ig) variable region, for identifying interactions between
CC an extracellular domain of a transmembrane protein and a polypeptide, for
CC high-throughput identification of compounds that inhibit phosphorylation
CC regulated signal transducers, forming a enzyme complementation system for
CC selecting simultaneous incorporation of multiple genetic elements into a
CC host cell and for activating a beta-lactam derivative of an antitumor
CC compound in a host who is in need of it. The present sequence represents
CC the *Escherichia coli* mature TEM-1 beta-lactamase, which is used in the
CC exemplification of the present invention
XX

XX Sequence 263 AA;
SQ

Query Match 100.0%; Score 975; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 6.6e-96;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFKVLLCGAVLSRID 60
DB 1 HPEITLVKVDADDOAGARVGYIELDINSKILLESFRPERPMMSTFKVLLCGAVLSRID 60
QY 61 AGQEQLGRRIRHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGSP 120
DB 61 AGQEQLGRRIRHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGSP 120
QY 121 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180
DB 121 KELTAFILNMGDHYTRLDRWPEBELNEAIPNDRDITMPVAAATTIRKLLTGELLTLASRQ 180

Qy 181 QLIDWMEADK 190
Db 181 QLIDWMEADK 190

RESULT 3
ADJ67709
ID ADJ67709 standard; protein; 263 AA.
XX
AC ADJ67709;

20-MAY-2004 (first entry)

Escherichia coli TEM-1 beta-lactamase.

fragment complementation system; marker protein;
multiple genetic element incorporation; antibiotic resistance;
beta-lactam derivative activation; anti-tumour compound;
functional assembly; protein-protein interaction; proteome interaction;
immunoglobulin variable region; immune cell protein; CD40;
phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
enzyme.

Escherichia coli.

US2004038317-A1.

26-FEB-2004.

22-SEP-2003; 2003US-00668778.

15-MAR-1999; 99US-0124339P.

25-MAY-1999; 99US-0135926P.

13-JAN-2000; 2000US-0175968P.

15-MAR-2000; 2000US-00526106.

(KALO-) KALOBIO INC.

Balint RF, Her J;

WPI; 2004-203222/19.

N-PSDB; ADJ67708.

Fragment complementation system for detecting immunoglobulin epitope, has
first oligopeptide containing N-terminal fragment with C-terminal break-
point, second oligopeptide containing C-terminal fragment with N-terminal
break-point.

Disclosure; SEQ ID NO 2; 47pp; English.

The invention describes a fragment complementation system (I) comprising
a first oligopeptide having an N-terminal fragment with a C-terminal
break-point, and a second oligopeptide having a C-terminal fragment with
a N-terminal break-point, where the N-terminal fragment and the C-
terminal fragment each are derived from a marker protein and the C-
terminal fragment is functionally reconstituted marker protein. (I) is useful for
selecting simultaneous incorporation of multiple genetic elements into a
host cell, and activating a beta-lactam derivative of an anti-tumour
compound in a host. The method described is useful for identifying a
second oligopeptide to which a first oligopeptide binds, involving co-
expressing the first and second oligopeptides. Binding of the first
oligopeptide to the second oligopeptide results in the functional
reassembly of the marker protein. The method is also useful for
monitoring the occurrence of protein-protein interactions in a sample;
identifying oligopeptide interactions between two different proteomes;
and identifying epitopes that bind to an immunoglobulin variable region.
(I) or an expression cassette (II), encoding a selectable N or C-terminal
peptide, is useful for identifying interactions between an extra cellular
domain of a transmembrane protein and a polypeptide, where the
transmembrane protein is an immune cell protein, preferably CD40. (I) or
(II) is useful for high-throughput identification of compound that
inhibit phosphorylation-regulated cell signal transducers. (I)

CC efficiently detects multiple interaction between extracellular and
CC intracellular protein with high throughput format. This is the amino acid
CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
CC used as a selectable gene in the fragment complementation system of the
CC invention.

Sequence 263 AA;

Query Match 100.0%; Score 975; DB 8; Length 263;
Best Local Similarity 100.0%; Pred. No. 6.6e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPETLVKVDADQLGARVGIIEIDLSNGKILSEFRPERFPMSSTFKYLICGAVLSRID 60
Db 1 HPETLVKVDADQLGARVGIIEIDLSNGKILSEFRPERFPMSSTFKYLICGAVLSRID 60

Qy 61 AQCEQLGRRIHYSQNDLVYFSPYTEKHLLTDGMTVRELCSAATITMSDNTNAILLTIGSP 120
Db 61 AQCEQLGRRIHYSQNDLVYFSPYTEKHLLTDGMTVRELCSAATITMSDNTNAILLTIGSP 120

Qy 121 KELTLPFLHMGDPVTRLDKWEPELNEAIPNDSRDITMPVAMATTLRKLTGELTLASRQ 180
Db 121 KELTLPFLHMGDPVTRLDKWEPELNEAIPNDSRDITMPVAMATTLRKLTGELTLASRQ 180

Qy 181 QLIDWMEADK 190
Db 181 QLIDWMEADK 190

RESULT 4
AAW16634
ID AAW16634 standard; protein; 264 AA.
XX
AC AAW16634;

09-AUG-1997 (first entry)

Beta-lactamase (including signal peptide).

Gene directed enzyme prodnug therapy; GDEPT;
virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;
HIV; inflammation.

Escherichia coli.

Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide

MO9719180-A2.

29-MAY-1997.

19-NOV-1996; 96WO-GB002845.

20-NOV-1995; 95GB-00023703.

(GLAX) GLAXO GROUP LTD.

Dev I, Moore JT, Ohmsted C;

WPI; 1997-298117/27.

N-PSDB; AAT66736.

Molecular chimera for gene or virus directed enzyme prodnug therapy -
useful for treatment of cancer, viral infection or inflammation.

Example; Page 28; 38pp; English.

Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
is the expression product of a molecular chimera, designated pcMV-BL
(AAT66737), in which the beta-lactamase gene is under control of the CMV
intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodrug into an agent toxic to the cell for
 CC treatment of cancer, viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 975; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 6,6e-98; Mismatches 0; Indels 0; Gaps 0;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDQGVYIEIDNSGKILSFRRPFRPMSSTFKYLICGAVLSRID 60

DB 2 HPEITLVKVDADQDQGVYIEIDNSGKILSFRRPFRPMSSTFKYLICGAVLSRID 61

QY 61 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120

DB 62 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 121

QY 121 KELTAFILNMGDHVTRLDRWPELNEALPNDERDTTTPVAAATTLTKLTGELTLASRQ 180

DB 122 KELTAFILNMGDHVTRLDRWPELNEALPNDERDTTTPVAAATTLTKLTGELTLASRQ 181

QY 181 QLIDWMEADK 190

DB 182 QLIDWMEADK 191

RESULT 5

AAW18680 AAW18680 standard; protein; 264 AA.

AAW18680;

13-AUG-1997 (first entry)

Intracellularly-expressed beta-lactamase.

Producing therapy; gene directed enzyme producing therapy; GDEPT;

virus directed enzyme producing therapy; VDEPT; lung cancer;

beta-lactamase; PCMV-delBL.

Escherichia coli.

MO9719183-A2.

29-MAY-1997.

19-NOV-1996; 96WO-GB002846.

20-NOV-1995; 95GB-00023703.

(GLAXO) GLAXO GROUP LTD.

Dev I, Moore JT, Sethna PB;

WPI, 1997-298118/27.

N-PSDB; AAT70311.

DNA construct for gene-directed enzyme producing therapy of lung cancer -

comprises lung- or neuroendocrine-specific promoter controlling

expression of prodrug-converting enzyme.

Example 811; Page 32-34; 53pp; English.

The intracellular form (AAW18680) of TEM beta-lactamase is expressed by

PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding

sequence, minus the signal sequence, is placed under control of the

intermediate/early promoter of cytomegalovirus. Intracellular beta-

lactamase constructs, placed under control of promoter/enhancer elements

of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in prodrug therapy of lung

CC cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 975; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 6,6e-98; Mismatches 0; Indels 0; Gaps 0;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQDQGVYIEIDNSGKILSFRRPFRPMSSTFKYLICGAVLSRID 60

DB 2 HPEITLVKVDADQDQGVYIEIDNSGKILSFRRPFRPMSSTFKYLICGAVLSRID 61

QY 61 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 120

DB 62 AGQQLGRIRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANILLTTIGCP 121

QY 121 KELTAFILNMGDHVTRLDRWPELNEALPNDERDTTTPVAAATTLTKLTGELTLASRQ 180

DB 122 KELTAFILNMGDHVTRLDRWPELNEALPNDERDTTTPVAAATTLTKLTGELTLASRQ 181

QY 181 QLIDWMEADK 190

DB 182 QLIDWMEADK 191

RESULT 6

AAW31575 AAW31575 standard; protein; 286 AA.

AAW31575;

10-MAR-2003 (revised)

04-JUN-1993 (first entry)

Ampicillin resistance protein.

CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

xenobiotics; circular; chimeric cytochrome P4501A1.

Homo sapiens.

US5180666-A.

19-JAN-1993.

27-JUN-1991; 91US-00721775.

27-JUN-1991; 91US-00721775.

(UYWA-) UNIV WAYNE STATE.

States JC, Hines RN, Novak RF;

WPI, 1993-052845/06.

N-PSDB; AAQ36498.

In vitro method for testing mutagenicity of a chemical - by metabolising

chemical cell line consisting of transformed fibroblasts having

detectable cytochrome P450 mixed function oxidase activity and detecting

gene damage.

Disclosure; Col 21-24; 24pp; English.

The expression constructs PRNH127 and PRNH155 contain identical sequences

but were constructed using different strategies (see AAQ36498). The

constructs comprise exons 2-7 of human CYP1A1 gene under the control of

the inducible mouse metallothionein (MT-1) promoter. The constructs also

contain an open reading frame in the opposite orientation to the

cytochrome P450 exons. This ORF encodes ampicillin resistance. The

constructs are suitable for transformation of human fibroblasts derived

from the xeroderma pigmentosum group A. Cultures of the transformed

fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKVDAEDQAGARVGYIELDLSGKILSPFPERPFPMSTFKVLLCGAVLSRD 60
DB 24 HPEITVKVDAEDQAGARVGYIELDLSGKILSPFPERPFPMSTFKVLLCGAVLSRD 83
QY 61 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGGDVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELITLASRQ 180
DB 144 KELTAFILNMGGDVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELITLASRQ 203
QY 181 QLIIDWMEADK 190
DB 204 QLIIDWMEADK 213

RESULT 7
AAR97619
ID AAR97619 standard; protein; 286 AA.

XX AAR97619;

DT 20-AUG-1996 (first entry)

DE Secretory beta-lactamase.

KM Gene therapy; gene directed enzyme prodnug therapy; GDEPT;
KM virus directed enzyme prodnug therapy; VDEPT; prodnug activation;
KM cytotoxic; cytosstatic; cancer; tumour; retrovirus; vector;
KM beta-lactamase; cephalosporin.

OS Synthetic.

FN W09616179-A1.

PD 30-MAY-1996.

PF 20-NOV-1995; 95WO-GB002716.

PR 18-NOV-1994; 94GB-00023367.

PA (WEILL) WEILLCOMB FOUND LTD.

PI Dev IK, Moore JT, Ohmstede C;

DR WPI: 1996-268615/27.

DR N-PSDB; AAT92920.

PT Molecular chimaera for use in enzyme gene therapy - is activated in a
PT target cell to express a secretible enzyme which cleaves a prodnug
PT outside the cell into a cytotoxic or cytostatic agent.

PS Example 3; Page 57-58; 73pp; English.

XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct
XX PCMV-BL (AAR97619), in which the beta-lactamase coding sequence is under
XX the control of the intermediate/early cytomegalovirus promoter. Beta-
XX lactamase delivery to mammalian cells confers sensitivity to
XX cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations
XX resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
XX of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
XX was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct
XX Sequence 286 AA;

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITVKVDAEDQAGARVGYIELDLSGKILSPFPERPFPMSTFKVLLCGAVLSRD 60
DB 24 HPEITVKVDAEDQAGARVGYIELDLSGKILSPFPERPFPMSTFKVLLCGAVLSRD 83
QY 61 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQLGRIIRHSQNDLVEYSPVTEKHLTDGKTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGGDVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELITLASRQ 180
DB 144 KELTAFILNMGGDVTRLDRWEPELNEAIPNDRDITMPVAMATTLRKLLTGELITLASRQ 203
QY 181 QLIIDWMEADK 190
DB 204 QLIIDWMEADK 213

RESULT 8
AAR96423
ID AAR96423 standard; protein; 286 AA.

XX AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

DE Cytochrome P450 (CYP1A1 construct).

KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;
KM metabolism.

OS Homo sapiens.

FN US5525482-A.

PD 11-JUN-1996.

PF 15-NOV-1994; 94US-00339658.

PR 27-JUN-1991; 91US-00721775.

PR 09-DEC-1992; 92US-00990295.

PA (UTWA-) UNIV WAYNE STATE.

PI Hines RN, Novak RF, States JC;

DR WPI: 1996-286397/29.

DR N-PSDB; AAT30354.

PT Testing chemicals for cytotoxicity to human by detecting gene damage -
PT using recombinant fibroblasts transformed with cytochrome P450 gene under
PT control of inducible promoter.

PS Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-
XX cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNH127 and
XX pRNH15, were isolated by different methods and which both had the same
XX sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
XX of humans to a chemical. The method comprises exposing human fibroblast
XX cells normally not including any cytochrome P450 activity to potentially
XX toxic chemicals. The cells having been transformed to express cytochrome
XX P450, under the control of a controllable promoter through the CYP1A1
XX gene, upon exposure to the chemical in vitro. The chemical is metabolised
XX intracellularly into a cytochrome metabolite by oxidation within the

CC fibroblasts through the intracellular cytochrome P450 mixed function
 CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
 CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
 CC -MAR-2003 to correct PF field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 975; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIELDLSGKLTIESRPERPERPMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKVKADBDQAGAVGYIELDLSGKLTIESRPERPERPMSTFVLLCGAVLSRID 83
 QY 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVRELCSAITSNDNTAANLLTTIGSP 120
 DB 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVRELCSAITSNDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVANAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVANAATTIRKLLTGELTLASRQ 203
 QY 181 QLIDWMEADK 190
 DB 204 QLIDWMEADK 213

RESULT 9

AAW16635
 ID AAW16635 standard; protein; 286 AA.

XX AAW16635;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (no signal peptide).

XX Gene directed enzyme prodnug therapy; GDEPT;
 KW virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;
 KW HIV; inflammation.

XX Escherichia coli.

XX WO9719180-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002845.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAX) GLAXO GROUP LTD.

XX Dev I, Moore JT, Ohmsted C;

XX WPI; 1997-298117/27.

XX N-PSDB; AAT66737.

XX Molecular chimaera for gene or virus directed enzyme prodnug therapy -
 XX useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 26; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,
 CC is the expression product of a molecular chimaera, designated pCMV-delBL
 CC (AAT66738), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional
 CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme prodnug therapy. Intracellular expression of the beta-lactamase in
 CC a targeted cell allows conversion of a prodnug into an agent toxic to
 CC the cell for treatment of cancer, viral (e.g. HIV) infection or
 CC inflammation

XX Sequence 286 AA;

Query Match 100.0%; Score 975; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGAVGYIELDLSGKLTIESRPERPERPMSTFVLLCGAVLSRID 60
 DB 24 HPEITLVKVKADBDQAGAVGYIELDLSGKLTIESRPERPERPMSTFVLLCGAVLSRID 83
 QY 61 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVRELCSAITSNDNTAANLLTTIGSP 120
 DB 84 AGOBOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVRELCSAITSNDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVANAATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWEPBELNEAIPNDRDITTMVANAATTIRKLLTGELTLASRQ 203
 QY 181 QLIDWMEADK 190
 DB 204 QLIDWMEADK 213

RESULT 10

AAW18679
 ID AAW18679 standard; protein; 286 AA.

XX AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodnug therapy; gene directed enzyme prodnug therapy; GDEPT;
 KW virus directed enzyme prodnug therapy; VDEPT; lung cancer;
 KW beta-lactamase; pCMV-BL.

XX Escherichia coli.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Protein /label= Sig_peptide

FT /label= Mat_protein

XX WO9719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAX) GLAXO GROUP LTD.

XX Dev I, Moore JT, Sethna PB;

XX WPI; 1997-298118/27.

XX N-PSDB; AAT70309.

XX DNA construct for gene-directed enzyme prodnug therapy of lung cancer -
 XX comprises lung- or neuroendocrine-specific promoter controlling
 XX expression of prodnug-converting enzyme.

XX Example 8ii; Page 26-27; 53pp; English.

XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-
 CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
 CC placed under control of the intermediate/early promoter of
 CC cytomagalovirus. Secretory beta-lactamase constructs, placed under
 CC control of promoter/enhancer elements of lung-associated protein or
 CC neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodng therapy of lung cancer
 XX Sequence 286 AA;
 SQ Query Match 100.0%; Score 975; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILSPRPFRPMSFFKVLICGAVLSRID 60
 |||||
 DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILSPRPFRPMSFFKVLICGAVLSRID 83
 QY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120
 DB 84 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMPVMAATTIRKLLTGSELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMPVMAATTIRKLLTGSELTLASRQ 203
 QY 181 OLIDWMEADK 190
 |||||
 DB 204 OLIDWMEADK 213

RESULT 11
 AAY08529
 ID AAY08529 standard; protein; 286 AA.
 XX AAY08529;
 AC AAY08529;
 XX 03-AUG-1999 (first entry)
 DT Vector pASK75 beta-1a protein.
 DE
 XX
 KW Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
 KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
 KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
 KW allergy.
 KM
 XX Synthetic.
 OS
 XX
 FN MO9925866-A1.
 XX
 PD 27-MAY-1999.
 XX
 XX 11-NOV-1998; 98WO-FI000873.
 PF
 XX 14-NOV-1997; 97FI-00004235.
 PR
 XX
 PA (KORP/) KORPELA M.
 PA (KARP/) KARP M.
 PA (KURI/) KURITTU J.
 PI
 XX Korpele M, Karp M, Kurittu J;
 XX WPI; 1999-338015/28.
 DR N-PSDB; AAV72418.
 DR
 XX
 PT Assaying for tetracycline using recombinant prokaryotic cells.
 PS
 PS Disclosure; Page 47-48; 67pp; English.

CC This invention describes a novel tetracycline assay that uses recombinant
 CC prokaryotic cells comprising a luciferase gene under the transcriptional
 CC control of a tetracycline repressor and tetracycline promoter and
 CC involves the detection of luminescence emitted from the cells. The assay
 CC can be used to distinguish tetracycline from other microbial agents. The
 CC invention also describes a novel plasmid comprising either the luxCDABE
 CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA)
 CC from Tn10, or the insect luciferase gene, a tetracycline repressor (TetR)
 CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
 CC method can be used for the determination of tetracycline in a sample,

CC e.g. to study the dosage and penetration of the medicine. The method can
 CC also be used to test cheese production, as cheese making bacteria are not
 CC able to work in the presence of tetracycline. The method can also be used
 CC to determine the presence or concentration of antibiotics in foodstuffs,
 CC e.g. for allergic people. The present assay method does not rely on the
 CC growth of microbes as do conventional tests, and so is much more rapid.
 CC The present assay is also more sensitive, as even a small amount of
 CC luminescence can be detected

XX Sequence 286 AA;
 SQ Query Match 100.0%; Score 975; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 7.4e-98;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGYIELDLSGKILSPRPFRPMSFFKVLICGAVLSRID 60
 |||||
 DB 24 HPEITLVKVDADQAGRVGYIELDLSGKILSPRPFRPMSFFKVLICGAVLSRID 83
 QY 61 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 120
 DB 84 AGOEOLGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMPVMAATTIRKLLTGSELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWPELNEAIPNDRDITTMPVMAATTIRKLLTGSELTLASRQ 203
 QY 181 OLIDWMEADK 190
 |||||
 DB 204 OLIDWMEADK 213

RESULT 12
 AAB10442
 ID AAB10442 standard; protein; 286 AA.
 XX AAB10442;
 AC AAB10442;
 XX 01-DEC-2000 (first entry)
 DT Expression vector pSEX15G2 bla protein.
 DE
 XX
 KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
 KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
 DT
 XX
 XX Synthetic.
 OS
 XX
 FN DE19900635-A1.
 XX
 PD 13-JUL-2000.
 PF
 XX 11-JAN-1999; 99DE-01000635.
 PR
 XX 11-JAN-1999; 99DE-01000635.
 PA (DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.
 PA Breilting F, Pouscka A, Moldenhauer G;
 XX WPI; 2000-499832/45.
 DR N-PSDB; AAA71430.
 DR
 XX
 PT Selecting monoclonal antibodies, by expressing them on the surface of
 PT hybridomas attached to antibody-binding protein, then reaction with
 PT antibody library.
 PS
 PS Claim 16; Fig 3; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
 CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
 CC cells to produce antibody-producing hybridomas such that the antibodies
 CC are presented at the surface of the hybridomas by an antibody-binding
 CC protein (I); and (ii) binding the antibody to antigens (Ag). The

CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(K)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select MAb with specificity for particular
CC antigens. MAb can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in MAb selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX11G2 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVDADQAGARVGYIELDNLSGKILSFRRPEERFPMWSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVDADQAGARVGYIELDNLSGKILSFRRPEERFPMWSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSDNTAANLLTTIGCP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHTRLDKRWPELNEAIPNDRDPTMVPAAATLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHTRLDKRWPELNEAIPNDRDPTMVPAAATLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.

AC AAB10438;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11L4 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Brettlung F, Poustka A, Moldenhauer G;

DR MPI: 2000-499832/45.
N-PSDB; AAA71428.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 1; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (MAb) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(K)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select MAb with specificity for particular
CC antigens. MAb can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in MAb selection. This sequence represents the Neo-R
CC protein contained in the expression vector pSEX11L4 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVDADQAGARVGYIELDNLSGKILSFRRPEERFPMWSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVDADQAGARVGYIELDNLSGKILSFRRPEERFPMWSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSDNTAANLLTTIGCP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATWSDNTAANLLTTIGCP 143
QY 121 KELTAFILNMGDHTRLDKRWPELNEAIPNDRDPTMVPAAATLRKLLTGELLTLASRQ 180
DB 144 KELTAFILNMGDHTRLDKRWPELNEAIPNDRDPTMVPAAATLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 14
AAB10440
ID AAB10440 standard; protein; 286 AA.

AC AAB10440;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Brettlung F, Poustka A, Moldenhauer G;

DR MPI: 2000-499832/45.
N-PSDB; AAA71429.

XX Selecting monoclonal antibodies, by expressing them on the surface of

PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I K(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX162 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPFRPFRPMMSTFKVLGCAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPFRPFRPMMSTFKVLGCAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 120
DB 84 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 143
QY 121 KELTAFLLNMGGHVTRLDRWPELNEALPNDERDTTTPVAMATTYRKLLTGLTLASRQ 180
DB 144 KELTAFLLNMGGHVTRLDRWPELNEALPNDERDTTTPVAMATTYRKLLTGLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 15

AAB50898
ID AAB50898 standard; protein; 286 AA.

AC AAB50898;

DT 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

KM bla resistance marker; recombinant host cell; saccharification;
KM fermentation; polysaccharase; oligosaccharide degradation; cel2 gene;
KM glucanase; integration vector; pLO12306.

OS Unidentified.

PN WO200071729-A2.

PD 30-NOV-2000.

PF 26-MAY-2000; 2000WO-US014773.

PR 26-MAY-1999; 99US-0136376P.

PA (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram IO, Zhou S;
XX
DR MPI: 2001-032043/04.
DR N-PSDB; AAC91455.

XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.
XX
PS Disclosure; Page 82-83; 87pp; English.

CC The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermenting processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the cel2 gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.4e-98;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSGKILSPFRPFRPMMSTFKVLGCAVLSRID 60
DB 24 HPEITLVKVDADQAGARVGYIELDLSGKILSPFRPFRPMMSTFKVLGCAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 120
DB 84 AGQEQLGRRIRHSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTTIGSP 143
QY 121 KELTAFLLNMGGHVTRLDRWPELNEALPNDERDTTTPVAMATTYRKLLTGLTLASRQ 180
DB 144 KELTAFLLNMGGHVTRLDRWPELNEALPNDERDTTTPVAMATTYRKLLTGLTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

Search completed: June 10, 2005, 10:49:12
Job time : 73.6679 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 19.4801 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975
Sequence: 1 HPEITLVKVDADQAGRVG.....GELTLASRQQLDWMKADK 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	100.0	286	1	US-07-721-775A-2
2	975	100.0	286	1	US-08-339-658-2
3	975	100.0	286	3	US-09-263-933-7
4	975	100.0	286	3	US-09-263-933-14
5	975	100.0	286	3	US-09-263-933-21
6	975	100.0	286	3	US-09-263-933-21
7	975	100.0	286	3	US-09-263-933-21
8	975	100.0	286	3	US-09-263-933-21
9	975	100.0	286	4	US-09-263-933-21
10	975	100.0	286	4	US-09-263-933-21
11	975	100.0	286	4	US-09-263-933-21
12	975	100.0	286	4	US-09-263-933-21
13	975	100.0	286	4	US-09-263-933-21
14	975	100.0	286	4	US-09-263-933-21
15	975	100.0	286	4	US-09-263-933-21
16	975	100.0	286	4	US-09-263-933-21
17	975	100.0	286	4	US-09-263-933-21
18	975	100.0	286	4	US-09-263-933-21
19	975	100.0	286	4	US-09-263-933-21
20	975	100.0	286	4	US-09-263-933-21
21	975	100.0	286	4	US-09-263-933-21
22	975	100.0	286	4	US-09-263-933-21
23	975	100.0	286	4	US-09-263-933-21
24	975	100.0	286	4	US-09-263-933-21
25	975	100.0	286	4	US-09-263-933-21
26	975	100.0	286	4	US-09-263-933-21
27	975	100.0	286	4	US-09-263-933-21

28	975	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	975	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	975	100.0	299	4	US-09-490-324-285	Sequence 298, App
31	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
32	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
33	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
34	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
35	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
36	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
37	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
38	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
39	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
40	975	100.0	299	4	US-09-490-324-285	Sequence 300, App
41	974	99.9	286	4	US-10-191-966-16	Sequence 2, Appl
42	974	99.9	286	4	US-10-191-966-16	Sequence 2, Appl
43	974	99.9	286	4	US-10-191-966-16	Sequence 2, Appl
44	974	99.9	286	4	US-10-191-966-16	Sequence 2, Appl
45	974	99.9	286	4	US-10-191-966-16	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-721-775A-2

Sequence 2, Application US/07721775A

Patent No. 5180666

GENERAL INFORMATION:

APPLICANT: States, J. Christopher

APPLICANT: Hines, Ronald N.

TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING

TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSER: Reising, Ethelington, Barnard, Perry & Milton

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: U.S.A.

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: PC-DOS/MS-DOS

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Releasee #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07721,775A

FILING DATE: 19910627

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-321WSU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (313) 689-3554

TELEFAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-721-775A-2

Query Match 100.0%; Score 975; DB 1; Length 286;

Best local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGRVGIELDINSKIIISRPFRPFMSTFKYLICAVLSRID 60

DB 24 HPEITLVKVDADQAGRVGIELDINSKIIISRPFRPFMSTFKYLICAVLSRID 83

QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFHNMGDHVTRLDRWPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHVTRLDRWPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QUIDMWEADK 190
DB 204 QUIDMWEADK 213

RESULT 2

US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5525482
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5525482ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Reising, Ethington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339.658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990.295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321MSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 100.0%; Score 975; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFRRPFRPPMSTFVYLICGAVLSRID 60
DB 24 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFRRPFRPPMSTFVYLICGAVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFHNMGDHVTRLDRWPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHVTRLDRWPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QUIDMWEADK 190
DB 204 QUIDMWEADK 213

RESULT 3

US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263.933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129.611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-7

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFRRPFRPPMSTFVYLICGAVLSRID 60
DB 24 HPEITLVKKADBDQAGAVGYIELDLSNGKILSFRRPFRPPMSTFVYLICGAVLSRID 83
QY 61 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTGGP 120
DB 84 AGOEOLGRIRHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFHNMGDHVTRLDRWPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFHNMGDHVTRLDRWPELNEAI PNDERDITMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QUIDMWEADK 190
DB 204 QUIDMWEADK 213

RESULT 4

US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263.933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129.611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-14

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDINSKILSFPRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGVGYIELDINSKILSFPRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMEADK 190
DB 204 QUIDMEADK 213

RESULT 5

US-09-263-933-21
Sequence 21, Application US/09263933
Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potte, Karen E.
APPLICANT: Jackson, Roderica L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-21

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDINSKILSFPRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGVGYIELDINSKILSFPRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMEADK 190
DB 204 QUIDMEADK 213

RESULT 6

US-09-025-769B-265
Sequence 265, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vlc

APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-265

Query Match 100.0%; Score 975; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDINSKILSFPRPFRPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGVGYIELDINSKILSFPRPFRPMSTFKVLLCGAVLSRID 83
QY 61 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOBLGRIRHYSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLLNMGDHYRLDRMBELNEAIPNDRDITMPVAAATTIRKLLTGELTLASRQ 203
QY 181 QUIDMEADK 190
DB 204 QUIDMEADK 213

RESULT 7

US-09-025-769B-362
Sequence 362, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vlc
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

PRIOR APPLICATION DATA:
FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000

TELEFAX: (212)596-9080

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-769B-362

Query Match 100.0%; Score 975; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADADQAGAVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADADQAGAVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAANLLTTIGSP 120
DB 84 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAANLLTTIGSP 143
QY 121 KeltaFLHMGDHYTRLDWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHMGDHYTRLDWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 8

US-09-919-901-7

Sequence 7, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

PRIOR FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patent In Ver. 2.0

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-7

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADADQAGAVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADADQAGAVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAANLLTTIGSP 120
DB 84 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAANLLTTIGSP 143
QY 121 KeltaFLHMGDHYTRLDWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHMGDHYTRLDWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 9

US-09-919-901-14

Sequence 14, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

PRIOR FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 14

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: :
US-09-919-901-14

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADADQAGAVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADADQAGAVGYIEIDLSNGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAANLLTTIGSP 120
DB 84 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAANLLTTIGSP 143
QY 121 KeltaFLHMGDHYTRLDWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHMGDHYTRLDWPEPELNEAIPNDRDPTMPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

Db 204 QUIDMMEADK 213

RESULT 10

US-09-919-901-21

; Sequence 21, Application US/09919901

; Patent No. 6599738

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patrick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

; FILE REFERENCE: 0125-0005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 09/263,933

; PRIOR FILING DATE: 1999-02-08

; PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR FILING DATE: 1998-08-05

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 286

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION:

US-09-919-901-21

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKYADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60

Db 24 HPELVKVKYADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTANILLTTIGSP 120

Db 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTANILLTTIGSP 143

QY 121 KELLTAFLINMGHVTRLRWEPELNEAIPNDRDITMPVAMATTTLRKLTGELLTLASRQ 180

Db 144 KELLTAFLINMGHVTRLRWEPELNEAIPNDRDITMPVAMATTTLRKLTGELLTLASRQ 203

QY 181 QUIDMMEADK 190

Db 204 QUIDMMEADK 213

RESULT 11

US-09-490-070A-265

; Sequence 265, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESSES:

; ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman

; ADDRESS: White & McLaughlin

; STREET: 1666 K Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20006

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070A

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Colin G. Sandercock, Esq.

; REGISTRATION NUMBER: 31,298

; REFERENCE/DOCKET NUMBER: 37629-0005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 912-2000

; TELEFAX: (202) 912-2020

; INFORMATION FOR SEQ ID NO: 265:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 100.0%; Score 975; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1e-107;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKYADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60

Db 24 HPELVKVKYADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTANILLTTIGSP 120

Db 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTANILLTTIGSP 143

QY 121 KELLTAFLINMGHVTRLRWEPELNEAIPNDRDITMPVAMATTTLRKLTGELLTLASRQ 180

Db 144 KELLTAFLINMGHVTRLRWEPELNEAIPNDRDITMPVAMATTTLRKLTGELLTLASRQ 203

QY 181 QUIDMMEADK 190

Db 204 QUIDMMEADK 213

RESULT 12

US-09-490-070A-362

; Sequence 362, Application US/09490070A

; Patent No. 6696248

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; APPLICANT: Pack, Peter

; APPLICANT: Ilag, Vic

; APPLICANT: Ge, Liming

; APPLICANT: Moroney, Simon

; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESSES:

; ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman

; ADDRESS: White & McLaughlin

; STREET: 1666 K Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDINSKILLESFRRPFRPMMSTFKVLGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYIELDINSKILLESFRRPFRPMMSTFKVLGAVLSRID 83
QY 61 AGOGLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOGLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFPHNMGDHYTRLDRWPELNEAI PNDERDTMPEVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFPHNMGDHYTRLDRWPELNEAI PNDERDTMPEVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOPPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDAEDQAGRVGYIELDINSKILLESFRRPFRPMMSTFKVLGAVLSRID 60
DB 24 HPELVKVKDAEDQAGRVGYIELDINSKILLESFRRPFRPMMSTFKVLGAVLSRID 83
QY 61 AGOGLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOGLGRRIHYSONDLVEYSPTVEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFPHNMGDHYTRLDRWPELNEAI PNDERDTMPEVAAATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFPHNMGDHYTRLDRWPELNEAI PNDERDTMPEVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMMEADK 190
DB 204 QLIDMMEADK 213

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOAGARVGYIELDLSNGKILSPFRERFPMSSTFKYLGCAYLSRID 60
DB 24 HPEITLVKVDADDOAGARVGYIELDLSNGKILSPFRERFPMSSTFKYLGCAYLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KETLAFILNMGDVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1e-107;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADDOAGARVGYIELDLSNGKILSPFRERFPMSSTFKYLGCAYLSRID 60
DB 24 HPEITLVKVDADDOAGARVGYIELDLSNGKILSPFRERFPMSSTFKYLGCAYLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 120

DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGVTRELCSAATMSDNTAANLLTTIGSP 143
QY 121 KETLAFILNMGDVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
DB 144 KETLAFILNMGDVTRLDRWPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
QY 181 QLIDWMEADK 190
DB 204 QLIDWMEADK 213

Search completed: June 10, 2005, 11:01:16
Job time : 20.4801 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 14.7307 Seconds

(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202

Perfect score: 1032

Sequence: 1 HPEITLVKVKADBDQAGRVG.....IDMWEADKVAGPLRSALPA 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 203416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 203416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1032	100.0	286	2	TS1301	Beta-lactamase (EC
2	1032	100.0	286	2	S47061	Beta-lactamase (EC
3	1032	100.0	286	4	S41975	Beta-lactamase (EC
4	1027	99.5	286	1	PNRCP	Beta-lactamase (EC
5	1027	99.5	286	4	I40905	Beta-lactamase (EC
6	1019	98.7	286	2	S30113	Beta-lactamase (EC
7	1014	98.3	286	2	S60312	extended spectrum
8	1013	98.2	286	2	S60310	extended spectrum
9	1013	98.2	286	2	S60311	Beta-lactamase (EC
10	1013	98.2	286	2	J01546	Bla protein - Salm
11	717	69.5	286	2	S16146	Beta-lactamase (EC
12	717	69.5	286	2	A60679	Beta-lactamase (EC
13	713	69.1	265	2	S00464	Beta-lactamase (EC
14	713	69.1	265	2	S02434	Beta-lactamase (EC
15	713	69.1	286	1	A44998	Beta-lactamase (EC
16	713	69.1	286	2	A60632	Beta-lactamase (EC
17	710	68.8	286	2	A60448	Beta-lactamase (EC
18	710	68.8	286	2	A37200	Beta-lactamase (EC
19	688.5	66.7	287	1	A44996	Beta-lactamase (EC
20	688	66.7	279	2	A24469	Beta-lactamase (EC
21	653	63.3	286	1	A44958	Beta-lactamase (EC
22	543	52.6	298	2	A41381	Beta-lactamase (EC
23	446.5	43.3	281	2	D95395	probable Beta lact
24	426.5	41.3	302	2	S35188	Beta-lactamase (EC
25	424	41.1	293	2	S04649	Beta-lactamase (EC
26	423.5	41.0	291	2	S42075	Beta-lactamase (EC
27	419.5	40.6	314	2	A54543	Beta-lactamase (EC
28	418.5	40.6	314	2	S06967	Beta-lactamase (EC
29	417.5	40.5	294	2	S16553	Beta-lactamase (EC

30	415.5	40.3	306	1	B45822	Beta-lactamase (EC
31	410.5	39.8	306	2	G69674	Beta-lactamase (EC
32	409.5	39.7	288	2	J01136	Beta-lactamase (EC
33	408.5	39.6	306	2	S47330	penicillinase - Ba
34	408	39.5	305	2	A61156	Beta-lactamase (EC
35	408	39.5	305	2	A57002	Beta-lactamase (EC
36	408	39.5	305	2	A60680	Beta-lactamase (EC
37	405.5	39.3	304	2	A49789	Beta-lactamase (EC
38	405.5	39.3	304	2	A35001	Beta-lactamase (EC
39	398.5	38.6	288	2	J50755	Beta-lactamase (EC
40	397.5	38.5	311	2	JN0520	Beta-lactamase (EC
41	395.5	38.3	291	2	JP0074	Beta-lactamase (EC
42	393.5	38.1	263	2	S23929	Beta-lactamase (EC
43	390	37.8	276	2	JH0268	Beta-lactamase (EC
44	389.5	37.7	311	1	S02714	Beta-lactamase (EC
45	388.5	37.6	305	1	C45822	Beta-lactamase (EC

ALIGNMENTS

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RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C.Accession: TS1301
R.WACH, A.; BRACHAT, A.; ALBERTSSEUT, C.; REBISCHUNG, C.; PHILIPPSEN, P.
Yeast 13, 1065-1075, 1997
A>Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A.Reference number: 209587
A.Accession: TS1301
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-286 <WAC>
A.Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
A.Genetics:
A.Gene: bla
A.Superfamily: beta-lactamase I
C.Keywords: hydrolase

Query Match      100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.2e-82;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPEITLVKVKADBDQAGRVGIIELDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 60
      |||
DB      24 HPEITLVKVKADBDQAGRVGIIELDLSGKILSFRRPFRPPMSTFVLLCGAVLSRID 83
QY      61 AGQEQIGRRIRHSQNDLVESGPTVEKHITDGMVPELCSAIIWSDNRAVLLTTIGSP 120
      |||
DB      84 AGQEQIGRRIRHSQNDLVESGPTVEKHITDGMVPELCSAIIWSDNRAVLLTTIGSP 143
QY      121 KELTAFILNMGDHYTRLDWPEPELNEAIPNDRDITTMVAAVTKRLITGLTLTASRQ 180
      |||
DB      144 KELTAFILNMGDHYTRLDWPEPELNEAIPNDRDITTMVAAVTKRLITGLTLTASRQ 203
QY      181 QIIDWEADKVAGPLRSALPA 202
      |||
DB      204 QIIDWEADKVAGPLRSALPA 225

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C.Species: phage phi-X174
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
A.Accession: S47061
R.Henrich, B.; Schmidtberger, B.
Submitted to the EMBL Data Library, July 1994
A.Description: A variant of phix174 gene E-based positive selection vectors with enhancec
A.Reference number: S47060
A.Accession: S47061

```


RESULT 5

140905 beta-lactamase (EC 3.5.2.6) - synthetic

C:Species: synthetic

A:Note: cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. cynod

C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000

C:Accession: 140905

R:Taylor, J.; Stearman, R.S.; Urciani, B.B.

A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.

A:Reference number: 140904; MUID:93361581; PMID:7689234

A:Accession: 140905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <RES>

A:Cross-references: EMBL:U21228; NID:9885956; PIDD:AAA70411.1; PID:9885958

C:Keywords: hydrolase

Query Match 99.5%; Score 1027; DB 4; Length 286;

Best Local Similarity 99.0%; Pred. No. 3,2e-82;

Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 24 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 120

DB 84 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 143

QY 121 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 180

DB 144 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 203

QY 181 QLIDMMEADKVAAGPLRSALPA 202

DB 204 QLIDMMEADKVAAGPLRSALPA 225

RESULT 6

S30113 beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCF04C:Species: *Klebsiella pneumoniae*

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: S30113

R:Madlat, C.; Lourenco-Vital, J.; Goussard, S.; Courvalin, P.

Mol. Gen. Genet. 235, 113-121, 1992

A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple

A:Reference number: S30112; MUID:93062798; PMID:1331747

A:Accession: S30113

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <MAB>

A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:943797; PIDD:CAA45828.1; PID:943798

C:Genetics:

A:Gene: bla(TEM-3)

A:Genome: plasmid

A:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase

Query Match 98.7%; Score 1019; DB 2; Length 286;

Best Local Similarity 98.0%; Pred. No. 1,6e-81;

Matches 198; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 24 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 120

DB 84 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 143

QY 121 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 180

DB 144 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 203

QY 181 QLIDMMEADKVAAGPLRSALPA 202

DB 204 QLIDMMEADKVAAGPLRSALPA 225

RESULT 7

S60312 extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*C:Species: *Klebsiella pneumoniae*

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60312

R:Chanal, C.; Poupart, M.C.; Sirot, D.; Labie, R.; Sirot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; MUID:93037315; PMID:1416873

A:Accession: S60312

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:9296955; PIDD:CAA46346.1; PID:9296956

C:Superfamily: beta-lactamase I

Query Match 98.3%; Score 1014; DB 2; Length 286;

Best Local Similarity 97.5%; Pred. No. 4,4e-81;

Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 24 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 120

DB 84 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 143

QY 121 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 180

DB 144 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 203

QY 181 QLIDMMEADKVAAGPLRSALPA 202

DB 204 QLIDMMEADKVAAGPLRSALPA 225

RESULT 8

S60310 extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*C:Species: *Klebsiella pneumoniae*

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60310

R:Chanal, C.; Poupart, M.C.; Sirot, D.; Labie, R.; Sirot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; MUID:93037315; PMID:1416873

A:Accession: S60310

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65252; NID:9296951; PIDD:CAA46344.1; PID:9296952

C:Superfamily: beta-lactamase I

Query Match 98.2%; Score 1013; DB 2; Length 286;

Best Local Similarity 97.5%; Pred. No. 5,4e-81;

Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60

DB 24 HPELVKVKADBDQAGAVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83

QY 61 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 120

DB 84 AGOBLGRRIRHSQNDLVESPVTEKHLTDGTVRELCSAAITMSDNTAANILLTTIGCP 143

QY 121 KELTAFLLNMGDHVTRLDRWPELNEALPNDERDTTMAPAAATTLRKLLTGELLTLASRQ 180

Db 84 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRLSALPA 202
Db 204 QLIDWMEADKVAGPLRLSALPA 225

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60311; F37392; F00498
R/Chanal, C.; Poupard, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60311
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CHA>
A/Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969
R/Toimasky, M.E.
Plasmid 24, 218-226, 1990
A/Title: Sequencing and expression of aadA, bla, and tnpR from the multi-resistance trans
A/Reference number: A37392; MUID:91172904; PMID:1965948
A/Accession: F37392
A/Molecule type: DNA
A/Residues: 1-32 <TOL>
A/Cross-references: GB:M5547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C/Genetics:
A:Gene: TEM-bla
C:Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 98.2%; Score 1013; DB 2; Length 286;
Best Local Similarity 97.5%; Pred. No. 5.4e-81;
Matches 197; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEVLVVKVKAEDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEVLVVKVKAEDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRLSALPA 202
Db 204 QLIDWMEADKVAGPLRLSALPA 225

RESULT 10
J01546
Bla protein - Salmonella typhimurium plasmid NTP16
N/Alternate names: beta lactamase homolog
C/Species: Salmonella typhimurium
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: J01546
R/Cannon, P.W.; Strike, P.
Plasmid 27, 220-230, 1992
A/Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A/Reference number: J01548; MUID:92383313; PMID:1325061
A/Accession: J01546
A/Status: translation not shown

A/Molecule type: DNA
A/Residues: 1-286 <CAN>
A/Cross-references: UNIPROT:Q8L2F9
C/Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 98.2%; Score 1013; DB 2; Length 286;
Best Local Similarity 98.0%; Pred. No. 5.4e-81;
Matches 198; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEVLVVKVKAEDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEVLVVKVKAEDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 120
Db 84 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 143
QY 121 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRLSALPA 202
Db 204 QLIDWMEADKVAGPLRLSALPA 225

RESULT 11

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N/Alternate names: beta-lactamase SHV2A
C/Species: Klebsiella pneumoniae
C/Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C/Accession: S16146; A35395; S18767
R/Podbielski, A.; Schoenling, J.; Melzer, B.; Wernatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A/Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV
A/Reference number: S16146; MUID:91237320; PMID:2033379
A/Accession: S16146
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <POD>
A/Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A/Experimental source: plasmid pZMP1
R/lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A/Title: Direct involvement of IS26 in an antibiotic resistance operon.
A/Reference number: A35395; MUID:90264317; PMID:2160941
A/Accession: A35395
A/Molecule type: DNA
A/Residues: 1-30, 'L', 32-286 <LEE>
A/Cross-references: GB:X62115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A/Experimental source: plasmid BMH77
C/Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 69.5%; Score 717; DB 2; Length 286;
Best Local Similarity 67.7%; Pred. No. 3.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

QY 2 PETLVVKVKAEDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
Db 23 PETLVVKVKAEDQAGRVGYIELDLSGKILSFRRPFRPMMSTFKVLLCGAVLSRID 82
QY 62 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 121
Db 83 AGOQLGRRIHYSQNDLVKSPVTEKHLTDGTVRELCSAAITMSDNTAANLLTTIGSP 142
QY 122 ELTAFLLHNMGDHVTRLDRWPEPELNEAIPNDRDPTTVPVAAATTLRKLLTGELLTLASRQ 181

Db 143 G|T|A|T|R|Q|I|G|D|N|V|R|L|D|R|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 202
Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 203 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 223

RESULT 12

A60679
beta-lactamase (EC 3.5.2.6) SHV-2 precursor - *Salmonella typhimurium* plasmid pHT1
C|Species: *Salmonella typhimurium*
C|Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C|Accession: A60679
R|Garbary-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.C.
A|Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A|Reference number: A60679; MUID:90351141; PMID:2201259
A|Accession: A60679
A|Status: not compared with conceptual translation
A|Molecule type: DNA
A|Residues: 1-286 <GAR>
A|Cross-references: GB:L47119; NID:9972890; PIDN:AAA75015.1; PID:9972891
C|Genetics:
A|Genome: plasmid
C|Superfamily: Beta-lactamase I
C|Keywords: antibiotic resistance; hydrolase
F|1-21|Domain: signal sequence #status predicted <SIG>

Query Match 69.5%; Score 717; DB 2; Length 286;
Best Local Similarity 67.7%; Pred. No. 3.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

Qy 2 P|E|T|V|K|V|D|A|E|D|Q|A|R|G|Y|I|E|L|D|N|S|G|I|E|S|F|P|R|E|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61
Db 23 P|Q|P|E|Q|I|K|S|Q|S|Q|S|G|R|V|G|M|E|D|L|A|S|G|R|T|L|A|R|A|D|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 82
Qy 62 G|Q|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|T|A|N|L|L|T|T|I|G|G|P 121
Db 83 G|D|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|S|A|N|L|L|T|A|V|G|P|A 142
Qy 122 E|L|T|A|F|L|H|M|G|H|V|R|L|D|R|E|P|E|L|N|E|A|I|P|N|R|D|R|D|T|T|P|V|A|A|T|T|K|L|T|G|E|L|L|T|A|S|R|Q 181
Db 143 G|L|T|A|F|L|R|Q|I|G|D|N|V|R|L|D|R|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 202
Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 203 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 223

RESULT 13

S00464
beta-lactamase (EC 3.5.2.6) class A - *Escherichia coli* plasmid p453
N|Alternate names: beta-lactamase P1T-2; beta-lactamase SHV-1
C|Species: *Escherichia coli*
C|Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
C|Accession: S00464
R|Barthelemy, M.; Peduzzi, J.; Labia, R.
A|Title: Complete amino acid sequence of p453-plasmid-mediated P1T-2 beta-lactamase (SHV)
A|Reference number: S00464; MUID:88268817; PMID:3260490
A|Accession: S00464
A|Molecule type: protein
A|Residues: 1-265 <BAR>
C|Genetics:
A|Genome: plasmid
C|Superfamily: beta-lactamase I
C|Keywords: antibiotic resistance; hydrolase

Query Match 69.1%; Score 713; DB 2; Length 265;
Best Local Similarity 67.7%; Pred. No. 7.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

Qy 2 P|E|T|V|K|V|D|A|E|D|Q|A|R|G|Y|I|E|L|D|N|S|G|I|E|S|F|P|R|E|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61
Db 2 P|Q|P|E|Q|I|K|S|Q|S|G|R|V|G|M|E|D|L|A|S|G|R|T|L|A|R|A|D|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61

Qy 62 G|Q|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|T|A|N|L|L|T|T|I|G|G|P 121
Db 62 G|D|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|S|A|N|L|L|T|A|V|G|P|A 121

Qy 122 E|L|T|A|F|L|H|M|G|H|V|R|L|D|R|E|P|E|L|N|E|A|I|P|N|R|D|R|D|T|T|P|V|A|A|T|T|K|L|T|G|E|L|L|T|A|S|R|Q 181
Db 122 G|L|T|A|F|L|R|Q|I|G|D|N|V|R|L|D|R|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 181

Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 182 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 202

RESULT 14

S02434
beta-lactamase (EC 3.5.2.6) SHV-2 - *Escherichia coli*
C|Species: *Escherichia coli*
C|Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C|Accession: S02434
R|Barthelemy, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R.
A|Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydrate
A|Reference number: S02434; MUID:88196385; PMID:3129309
A|Accession: S02434
A|Molecule type: protein
A|Residues: 1-265 <BAR>
C|Superfamily: beta-lactamase I
C|Keywords: antibiotic resistance; hydrolase

Query Match 69.1%; Score 713; DB 2; Length 265;
Best Local Similarity 67.7%; Pred. No. 7.9e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

Qy 2 P|E|T|V|K|V|D|A|E|D|Q|A|R|G|Y|I|E|L|D|N|S|G|I|E|S|F|P|R|E|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61
Db 2 P|Q|P|E|Q|I|K|S|Q|S|G|R|V|G|M|E|D|L|A|S|G|R|T|L|A|R|A|D|R|F|P|M|S|T|F|K|V|L|G|C|A|V|L|R|D|A 61

Qy 62 G|Q|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|T|A|N|L|L|T|T|I|G|G|P 121
Db 62 G|D|E|Q|R|R|I|H|Y|S|O|N|D|V|E|S|P|V|T|E|K|H|L|D|G|M|T|V|R|E|L|C|S|A|I|T|S|D|N|S|A|N|L|L|T|A|V|G|P|A 121

Qy 122 E|L|T|A|F|L|H|M|G|H|V|R|L|D|R|E|P|E|L|N|E|A|I|P|N|R|D|R|D|T|T|P|V|A|A|T|T|K|L|T|G|E|L|L|T|A|S|R|Q 181
Db 122 G|L|T|A|F|L|R|Q|I|G|D|N|V|R|L|D|R|E|T|E|L|N|E|A|L|P|G|D|A|R|D|T|T|P|A|S|M|A|T|L|R|K|L|T|S|Q|R|S|A|R|S|Q|R|Q 181

Qy 182 L|I|D|W|E|A|D|K|V|A|G|P|L|R|S|A|L|P|A 202
Db 182 L|I|Q|W|V|D|R|V|A|G|P|L|R|S|V|L|P|A 202

RESULT 15

A44998
beta-lactamase (EC 3.5.2.6) SHV-2 - *Klebsiella ozaenae* plasmid pBP60
C|Species: *Klebsiella ozaenae*
C|Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C|Accession: A44998; S12703
R|Huletsky, A.; Couture, F.; Levesque, R.C.
A|Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.
A|Reference number: A44998; MUID:91136192; PMID:2285285
A|Accession: A44998
A|Molecule type: DNA
A|Status: preliminary
A|Cross-references: UNIPROT:P14558; GB:M95179; NID:9150488; PIDN:AAA25526.1; PID:9150489
R|Podiletski, A.; Melzer, B.
A|Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2))
A|Reference number: S12703; MUID:90370479; PMID:2395654

A:Accession: S12703
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790
C:Genetics:
A:Genome: plasmid
C:Superfamily: Beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 69.1%; Score 713; DB 1; Length 286;
Best Local Similarity 67.7%; Pred. No. 8.7e-55;
Matches 136; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

```
QY      2 PETLVKVDADQDQCARVGYIELDNGKILESFRPERFPMSTPKYLCAVLSRIDA 61
      | : : : | | | | | : : : | : : | : | : | : | : | : |
Db      23 PQLPQITLSQSLSGRVGMTEMDLASGRITLAWRADERFPMSTFKVVLCAVLAQVDA 82
      | : : : | | | | | : : : | : : | : | : | : | : | : |
QY      62 GQEQIGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTGGPK 121
      | : : : | | | | | : : : | : : | : | : | : | : | : |
Db      83 GDEQLERKIHRYRQDDVDYSPVSEKHLADGMTVGELCAAITMSDNSAANLLLATVGGPA 142
      | : : : | | | | | : : : | : : | : | : | : | : | : |
QY      122 ELTAPLHMGDPVTRLDNWEPELNEAIPNDERDITMPVMAATTLRKILTGELTLASRQ 181
      | : : : | | | | | : : : | : : | : | : | : | : | : |
Db      143 GLTAPLRLQIGNVTRLDNWEPELNEALPGDARDITTPASMAATLRLKILTSQRLSARSRQ 202
      | : : : | | | | | : : : | : : | : | : | : | : | : |
QY      182 LIDWWEADKVAGPILRSALPA 202
      | : : : | | | | | : : : | : : | : | : | : | : | : |
Db      203 LIDWWEADKVAGPILRSVLP 223
      | : : : | | | | | : : : | : : | : | : | : | : | : |
```

Search completed: June 10, 2005, 10:58:48
Job time : 15.7307 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 13.8556 Seconds

(without alignments)
1319.408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_190

Perfect score: 975

Sequence: 1 HPELTIVKVKDADQIGARVGV.....GELTLASRQQLIDWMEADK 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	286	2	T51301
2	975	100.0	286	2	S47061
3	975	100.0	286	4	S41975
4	970	99.5	286	1	PNRCP
5	970	99.5	286	4	I40905
6	962	98.7	286	2	S30113
7	957	98.2	286	2	S60312
8	956	98.1	286	2	S60310
9	956	98.1	286	2	S60311
10	956	98.1	286	2	J01546
11	956	98.1	286	2	S16146
12	666	68.3	286	2	A60679
13	662	67.9	286	2	S00464
14	662	67.9	286	2	S02434
15	662	67.9	286	1	A44958
16	662	67.9	286	2	A60632
17	659	67.6	286	2	A60448
18	659	67.6	286	2	A37200
19	644	66.1	279	2	A24469
20	637.5	65.4	287	1	A44966
21	611	62.7	286	1	A44958
22	523	53.6	298	2	A41381
23	431.5	44.3	281	2	D95395
24	410.5	42.1	314	2	D95697
25	407.5	41.8	294	2	S16553
26	406	41.6	293	2	S04649
27	401.5	41.2	263	2	A54543
28	401.5	41.2	302	2	S36188
29	400.5	41.1	306	1	B45822

30	398.5	40.9	291	2	S42075	beta-lactamase (EC
31	395.5	40.6	306	2	G69674	beta-lactamase (EC
32	390.5	40.1	311	2	JN0520	beta-lactamase (EC
33	389.5	39.9	306	2	S47330	penicillinase - Ba
34	381	39.1	305	2	A61156	beta-lactamase (EC
35	381	39.1	305	2	A57002	beta-lactamase (EC
36	381	39.1	305	2	A60680	beta-lactamase (EC
37	380.5	39.0	291	2	JP0074	beta-lactamase (EC
38	378.5	38.8	263	2	S23929	beta-lactamase (EC
39	373.5	38.3	305	1	C45822	beta-lactamase (EC
40	372	38.2	310	2	JU0091	beta-lactamase (EC
41	371.5	38.1	288	1	Q01136	beta-lactamase (EC
42	371.5	38.1	311	1	S02714	beta-lactamase (EC
43	367.5	37.7	304	2	A49789	beta-lactamase (EC
44	367.5	37.7	304	2	A35001	beta-lactamase (EC
45	366.5	37.6	307	1	PNBSL	beta-lactamase (EC

ALIGNMENTS

RESULT 1

T51301 beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000

C:Accession: T51301

R:WACH, A.; BRACHAT, A.; ALBERTSSEGUI, C.; REBSCHUNG, C.; PHILIPSEN, P.

Yeast 13, 1065-1075, 1997

A:Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharom

A:Reference number: Z09587

A:Accession: T51301

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <MAC>

A:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1

C:Genetics:

A:Gene: bla

C:Superfamily: beta-lactamase I

C:Keywords: hydrolase

Query Match 100.0%, Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HPELTIVKVKDADQIGARVGYIELDNGSKILIESRPERFRPMSTFKVLGAVLSRID	60
DB	24	HPELTIVKVKDADQIGARVGYIELDNGSKILIESRPERFRPMSTFKVLGAVLSRID	83
QY	61	AGQEQGRRIHYSQNDIVESFVTEKHLTDGWTVEELCSAATMSDNFANLLTTIGSP	120
DB	84	AGQEQGRRIHYSQNDIVESFVTEKHLTDGWTVEELCSAATMSDNFANLLTTIGSP	143
QY	121	KELTAFILHMGDVTIRLDRMEPELNEAIPNDRDITMPVAAATTKLITGELTLASRQ	180
DB	144	KELTAFILHMGDVTIRLDRMEPELNEAIPNDRDITMPVAAATTKLITGELTLASRQ	203
QY	181	QLIDWMEADK 190	
DB	204	QLIDWMEADK 213	

RESULT 2

S47061 beta-lactamase (EC 3.5.2.6) - phage phi-X174

C:Species: phage phi-X174

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S47061

R:Henrich, B.; Schmidberger, B.

Submitted to the EMBL Data Library, July 1994

A:Description: A variant of phix174 gene B-based positive selection vectors with enhancer

A:Reference number: S47060

A:Accession: S47061

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HEN>
A:Cross-references: UNIPROT:038058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209
C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 100.0%; Score 975; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILIESFRPERPMMSTPFVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDINSKILIESFRPERPMMSTPFVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANILLTTIGCP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANILLTTIGCP 143
QY 121 KETLTAFLNMGDHVTRLDRWPELNEALPNDERDITTMVMAATTIRKLLTGELTLASRQ 180
DB 144 KETLTAFLNMGDHVTRLDRWPELNEALPNDERDITTMVMAATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADK 190
DB 204 OLIDWMEADK 213

RESULT 3
S41975
beta-lactamase (EC 3.5.2.6) precursor - synthetic
C:Species: synthetic
C:Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_change 20-Oct-2000
R:Accession: S41975
R:Accession: K.H.; Montroll, L.; Kern, H.; Thulke, M.; Schutz, G.
Gene 148; 67-70, 1994
A:Title: Universal beta-galactosidase cloning vectors for promoter analysis and gene tar
A:Reference number: A57991; MUID:95011660; PMID:7926839
A:Accession: S41975
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <KAS>
A:Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1; PID:g453623
A:Note: submitted to the EMBL Data Library, December 1993
C:Keywords: hydrolase

Query Match 100.0%; Score 975; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 5.8e-80;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILIESFRPERPMMSTPFVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDINSKILIESFRPERPMMSTPFVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANILLTTIGCP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANILLTTIGCP 143
QY 121 KETLTAFLNMGDHVTRLDRWPELNEALPNDERDITTMVMAATTIRKLLTGELTLASRQ 180
DB 144 KETLTAFLNMGDHVTRLDRWPELNEALPNDERDITTMVMAATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADK 190
DB 204 OLIDWMEADK 213

RESULT 4
PNECP
beta-lactamase (EC 3.5.2.6) precursor - Escherichia coli plasmid
N:Alternate names: beta-lactamase TEM-6 (for Dlat-6 DNA); penicillinase
C:Species: Escherichia coli
C:Date: 30-Nov-1980 #sequence_revision 01-Sep-1981 #text_change 16-Aug-2004

C:Accession: A93821; A93820; A35387; S24415; A01005
R:Sucliff, J.G.
Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978
A:Title: Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid
A:Reference number: A93821; MUID:75012484; PMID:358200
A:Accession: A93821

A:Molecule type: DNA
A:Residues: 1-286 <STU>
A:Cross-references: UNIPROT:P00810; GB:V00613; GB:J01832; NID:g43710; PIDN:CAA23886.1; P1
A:Experimental source: plasmid pBR322

R:Ambler, R.P.; Scott, G.K.
Proc. Natl. Acad. Sci. U.S.A. 75, 3732-3736, 1978
A:Title: Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid f
A:Reference number: A93820; MUID:75012483; PMID:358199
A:Accession: A93820

A:Molecule type: protein
A:Residues: 24-36, 'K', 38-286 <AMB>
A:Experimental source: plasmid R6K
R:Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
J. Bacteriol. 172, 3040-3050, 1990
A:Title: The kil-hor regulation of broad-host-range plasmid RK2: nucleotide sequence, polype
A:Reference number: A35387; MUID:90264294; PMID:2160936
A:Accession: A35387

A:Molecule type: DNA
A:Residues: 182-286 <ROR>
A:Cross-references: GB:M32794; NID:g152521; PIDN:AAA26408.1; PID:g152522
A:Experimental source: PK2
R:Goussard, S.; Sougakoff, W.; Mabilat, C.; Bauernfeind, A.; Courvalin, P.
U. Gen. Microbiol. 137, 2681-2687, 1991
A:Title: An ISI-like element is responsible for high-level synthesis of extended-spectrum
A:Reference number: S24415; MUID:92166702; PMID:1665171
A:Accession: S24415

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-101, 'K', 103-161, 'H', 163-286 <GOU>
A:Cross-references: EMBL:X57972; NID:g41816; PIDN:CAA41038.1; PID:g41817
A:Experimental source: ISI-like blaT-6 DNA
R:Sucliff, J.G.
Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
A:Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.

A:Reference number: A80923; MUID:80002802; PMID:383387
A:Contents: annotation
C:Comment: like most penicillinases from gram-negative bacteria, this enzyme, coded by a
C:Genetics:
A:Genome: plasmid
A:Superfamily: Beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase; membrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-286/Product: beta-lactamase #status experimental <MAT>
F:68/Active site: Ser #status predicted
F:75-121/Diulfide bonds: #status predicted

Query Match 99.5%; Score 970; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 1.6e-79;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGAVGYIELDINSKILIESFRPERPMMSTPFVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGAVGYIELDINSKILIESFRPERPMMSTPFVLLCGAVLSRID 83
QY 61 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANILLTTIGCP 120
DB 84 AGOBLGRRIHYSQNDLVEYSPVTEKHLTDGMTVELCSAATMSDNTAANILLTTIGCP 143
QY 121 KETLTAFLNMGDHVTRLDRWPELNEALPNDERDITTMVMAATTIRKLLTGELTLASRQ 180
DB 144 KETLTAFLNMGDHVTRLDRWPELNEALPNDERDITTMVMAATTIRKLLTGELTLASRQ 203
QY 181 OLIDWMEADK 190
DB 204 OLIDWMEADK 213

RESULT 5

140905 beta-lactamase (EC 3.5.2.6) - synthetic

C:Species: synthetic

A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. cynod

C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000

C:Accession: 140905

R:Taylor, J.; Stearman, R.S.; Urcatani, B.B.

Plasmid 29, 241-244, 1993

A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.

A:Reference number: 140904; PMID:93361581; PMID:7689234

A:Accession: 140905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <RES>

A:Cross-references: EMBL:U21228; NID:9885956; PIND:AAA70411.1; PID:9885958

C:Keywords: hydrolase

Query Match 99.5%; Score 970; DB 4; Length 286;

Best Local Similarity 98.9%; Pred. No. 1.6e-79;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 60

Db 24 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFLLNMGDHYRLDRWPELNEALPNDERDTTMAPAAATTIRKLLTGLTLASRQ 180

Db 144 KELTAFLLNMGDHYRLDRWPELNEALPNDERDTTMAPAAATTIRKLLTGLTLASRQ 203

Qy 181 QLIDMMEADK 190

Db 204 QLIDMMEADK 213

RESULT 6

530113 beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCF04C:Species: *Klebsiella pneumoniae*

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: S30113

R:Mabilat, C.; Lourencao-Vital, J.; Gousard, S.; Courvalin, P.

Mol. Gen. Genet. 235, 113-121, 1992

A:Title: A new example of physical linkage between Tnl and Tn21: the antibiotic multiple

A:Reference number: S30112; PMID:93062798; PMID:1331747

A:Accession: S30113

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <MAB>

A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PIND:CAA45828.1; PID:g43798

C:Genetics:

A:Gene: bla(TEM-3)

A:Genome: plasmid

A:Superfamily: beta-lactamase I

C:Keywords: antibiotic resistance; hydrolase

Query Match 98.7%; Score 962; DB 2; Length 286;

Best Local Similarity 97.9%; Pred. No. 8.6e-79;

Matches 186; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 60

Db 24 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFLLNMGDHYRLDRWPELNEALPNDERDTTMAPAAATTIRKLLTGLTLASRQ 180

Db 144 KELTAFLLNMGDHYRLDRWPELNEALPNDERDTTMAPAAATTIRKLLTGLTLASRQ 203

Qy 181 QLIDMMEADK 190

Db 204 QLIDMMEADK 213

RESULT 7

560312 extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*C:Species: *Klebsiella pneumoniae*

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60312

R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; PMID:93037315; PMID:1416873

A:Accession: S60312

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:g296955; PIND:CAA46346.1; PID:g296956

C:Superfamily: beta-lactamase I

Query Match 98.2%; Score 957; DB 2; Length 286;

Best Local Similarity 97.4%; Pred. No. 2.4e-78;

Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 60

Db 24 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFLLNMGDHYRLDRWPELNEALPNDERDTTMAPAAATTIRKLLTGLTLASRQ 180

Db 144 KELTAFLLNMGDHYRLDRWPELNEALPNDERDTTMAPAAATTIRKLLTGLTLASRQ 203

Qy 181 QLIDMMEADK 190

Db 204 QLIDMMEADK 213

RESULT 8

560310 extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*C:Species: *Klebsiella pneumoniae*

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999

C:Accession: S60310

R:Chanal, C.; Poupart, M.C.; Strot, D.; Labia, R.; Strot, J.; Cluzel, R.

Antimicrob. Agents Chemother. 36, 1817-1820, 1992

A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.

A:Reference number: S60310; PMID:93037315; PMID:1416873

A:Accession: S60310

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65252; NID:g296951; PIND:CAA46344.1; PID:g296952

C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 956; DB 2; Length 286;

Best Local Similarity 97.4%; Pred. No. 3e-78;

Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 60

Db 24 HPEITLVKVKADBDQAGAVGYIELDLSGKILLESFRPERPMMSTPFVLLCGAVLSRD 83

Qy 61 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOEOLGRRIHSQNDLVYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGSP 143

Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 203
QY 181 QLIDWMEADK 190
Db 204 QLIDWMEADK 213

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C:Species: Klebsiella pneumoniae
C:Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S60311, F37392, F00498
R:Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60311
A:Status: preliminary; translation not shown
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <CHA>
A:Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969
R:Totmaeky, M.B.
Plasmid 24, 218-226, 1990
A:Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans
A:Reference number: A57392; MUID:91172904; PMID:1963948
A:Accession: F37392
A:Molecule type: DNA
A:Residues: 1-32 <TOL>
A:Cross-references: GB:M5547; NID:g155010; PIDN:AAA98408.1; PID:g155016
C:Genetics:
A:Gene: TEM-bla
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.1%; Score 956; DB 2; Length 286;
Best Local Similarity 97.4%; Pred. No. 3e-78; 2; Indels 0; Gaps 0;
Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDDQCARVGYITELDINSKILLESFRPERPFPMSSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKKAEDDQCARVGYITELDINSKILLESFRPERPFPMSSTFKVLLCGAVLSRD 83
QY 61 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 203
QY 181 QLIDWMEADK 190
Db 204 QLIDWMEADK 213

RESULT 10
J01546
bla protein - Salmonella typhimurium plasmid NTP16
N:Alternate names: beta lactamase homolog
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: J01546
R:Canon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
A:Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A:Reference number: J01538; MUID:9238313; PMID:132061
A:Accession: J01546
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-286 <CAN>
A:Cross-references: UNIPROT:Q8L2F9
C:Genetics:
A:Genome: plasmid
C:Superfamily: beta-lactamase I

Query Match 98.1%; Score 956; DB 2; Length 286;
Best Local Similarity 97.9%; Pred. No. 3e-78;
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDDQCARVGYITELDINSKILLESFRPERPFPMSSTFKVLLCGAVLSRD 60
Db 24 HPEITLVKKAEDDQCARVGYITELDINSKILLESFRPERPFPMSSTFKVLLCGAVLSRD 83
QY 61 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 120
Db 84 AGOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 143
QY 121 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 180
Db 144 KETLAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 203
QY 181 QLIDWMEADK 190
Db 204 QLIDWMEADK 213

RESULT 11

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N:Alternate names: beta-lactamase SHV2A
C:Species: Klebsiella pneumoniae
C:Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C:Accession: S16146, A35395, S18767
R:Podolski, A.; Schoenling, U.; Welzer, B.; Wernatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A:Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SH
A:Reference number: S16146; MUID:91237320; PMID:2033379
A:Accession: S16146
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <POD>
A:Cross-references: EMBL:X53817; NID:g43795; PIDN:CAA37813.1; PID:g43796
A:Experimental source: plasmid pZMP1
R:Lee, K.Y.; Hopkins, J.D.; Syvanen, M.
J. Bacteriol. 172, 3229-3236, 1990
A:Title: Direct involvement of IS26 in an antibiotic resistance operon.
A:Reference number: A35395; MUID:90264317; PMID:2160941
A:Molecule type: DNA
A:Residues: 1-30, 'L', 32-286 <LEE>
A:Cross-references: GB:X52115; NID:g48988; PIDN:CAA44025.1; PID:g48990
A:Experimental source: plasmid BW77
C:Genetics:
A:Gene: blaS2A
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 68.3%; Score 666; DB 2; Length 286;
Best Local Similarity 66.7%; Pred. No. 3.1e-52;
Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;

QY 2 PETLVKVDADQCARVGYITELDINSKILLESFRPERPFPMSSTFKVLLCGAVLSRD 61
Db 23 PETLVKVDADQCARVGYITELDINSKILLESFRPERPFPMSSTFKVLLCGAVLSRD 82
QY 62 GOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 121
Db 83 GOBLGRRIHYSQNDLVKSPVTEKHLTDGVTARELCSAAITMSDNTAAILTTIGSP 142
QY 122 ELTAFILNMGDHVTRLDRWPEPELNEALPNDERDITMPVAAATTLRKLLTGELITLASRQ 181

A/Accession: S12703
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <POD>
A/Cross-references: EMBL:X53433, NID:g43789, PIDN:CAA37524.1, PID:g43790
C/Genetics:
A/Genome: plasmid
C/Superfamily: Beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 67.9%; Score 662; DB 1; Length 286;

Best local Similarity 66.7%; Pred. No. 7.1e-52;

Matches 126; Conservative 28; Mismatches 35; Indels 0; Gaps 0;

```
QY      2 PETLVKVDADDOICARVGYTELDLNSGKILESFRPERFPMSTPKYLGCATLSRIDA 61
      |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      23 PQLPQLKLSQSLSGRVGMLEMDLADGRTLTAMRADERFPMSTPKVVLGAVLARVDA 82
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      62 GOEQLGRRIHYSNDLVEYSPVTEKHLTDGMTVRELCSAITMSDNTAANLLTTGGPK 121
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      83 GDEQLERKIHYRQDLVDYSPVSEKHLADGMTVGELCAAITMSDNSAANLLLATVGGPA 142
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      122 ELTAFLNMGDVTRLDRWEPELANEAIPNDBDPTMPVMAATTLRKLLTGELTLASRQ 181
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      143 GLTAFLRQIGDVTRLDRWETELNEALPGDARDTTTPASMAATLRLKLLTSQRLSARSQR 202
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      182 LIDWMEADK 190
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      203 LLQMMVDDK 211
```

Search completed: June 10, 2005, 10:58:47
Job time : 13.8556 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:22:36 ; Search time 78.3206 Seconds
(without alignments)
997.510 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202
Perfect score: 1032
Sequence: 1 HPTLVKVKADAEQDQGARVG.....IDWNEADRVAGPLRLSALPA 202

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	263	4	AAE05544 E. coli m
2	1032	100.0	263	4	AAE05544 E. coli m
3	1032	100.0	263	8	ADJ67709 Escherich
4	1032	100.0	264	2	AAW16634 Beta-lact
5	1032	100.0	264	2	AAW16634 Beta-lact
6	1032	100.0	264	2	AAW16634 Beta-lact
7	1032	100.0	264	2	AAW16634 Beta-lact
8	1032	100.0	264	2	AAW16634 Beta-lact
9	1032	100.0	264	2	AAW16634 Beta-lact
10	1032	100.0	264	2	AAW16634 Beta-lact
11	1032	100.0	264	2	AAW16634 Beta-lact
12	1032	100.0	264	2	AAW16634 Beta-lact
13	1032	100.0	264	2	AAW16634 Beta-lact
14	1032	100.0	264	2	AAW16634 Beta-lact
15	1032	100.0	264	2	AAW16634 Beta-lact
16	1032	100.0	264	2	AAW16634 Beta-lact
17	1032	100.0	264	2	AAW16634 Beta-lact
18	1032	100.0	264	2	AAW16634 Beta-lact
19	1032	100.0	264	2	AAW16634 Beta-lact
20	1032	100.0	264	2	AAW16634 Beta-lact
21	1032	100.0	264	2	AAW16634 Beta-lact
22	1032	100.0	264	2	AAW16634 Beta-lact
23	1032	100.0	264	2	AAW16634 Beta-lact
24	1032	100.0	264	2	AAW16634 Beta-lact
25	1032	100.0	264	2	AAW16634 Beta-lact

26	1032	100.0	290	4	AAW84362 Human imm
27	1032	100.0	327	2	AAW16636 Beta-lact
28	1032	100.0	327	2	AAW16636 Beta-lact
29	1032	100.0	408	6	ABR55981 hCG beta-
30	1032	100.0	585	6	ADJ67747 Beta-lact
31	1032	100.0	1031	5	ADJ46109 Single st
32	1032	100.0	1088	2	AAW88636 Plasmid p
33	1032	100.0	1277	2	AAW52701 Plasmid p
34	1032	100.0	2307	3	AAW70064 Recombina
35	1032	100.0	2307	3	AAW70065 Recombina
36	1032	100.0	2307	3	AAW70066 Recombina
37	1032	100.0	2761	2	ADH11249 Verrebrat
38	1031	99.9	286	2	AAW06551 Escherich
39	1031	99.9	872	7	ADK65686 E coli c1
40	1031	99.9	1293	7	ADK22811 Human G p
41	1031	99.9	1293	7	ADH14284 Vector pC
42	1031	99.9	1967	6	ABW82793 Amino aci
43	1027	99.5	265	2	AAW08234 E. coli R
44	1027	99.5	265	2	AAW08232 E. coli R
45	1027	99.5	265	2	AAW48613 Escherich

ALIGNMENTS

RESULT 1	AAE05544	AAE05544 standard; protein; 263 AA.
ID	AAE05544	standard; protein; 263 AA.
XX	AAE05544;	
AC	AAE05544;	
XX	AAE05544;	
DT	24-SEP-2001	(first entry)
XX	24-SEP-2001	(first entry)
DE	E. coli mature TEM-1 beta-lactamase.	
XX	E. coli mature TEM-1 beta-lactamase.	
KW	Interactio-dependent enzyme associatio; IdeA system; biosensor;	
KW	interarily permutated interaction-activated protein; marker protein;	
KW	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;	
KW	therapeutic; drug screening; thiodoxin; ampicillin resistance.	
OS	Escherichia coli.	
XX	Escherichia coli.	
XX	Escherichia coli.	
Key	Location/Qualifiers	
FT	Cleavage-site	27..28
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Region	36..40
FT	Region	/note="Inter-sub-domain loop"
FT	Cleavage-site	38..39
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Active-site	45
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Cleavage-site	74..75
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Cleavage-site	149..150
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Cleavage-site	172..173
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Region	189..204
FT	Region	/note="Inter-sub-domain loop"
FT	Cleavage-site	190..191
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Cleavage-site	202..203
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
FT	Cleavage-site	228..229
FT	Cleavage-site	/note="Break-point between alpha and omega fragments"
XX	WO200151629-A2.	
XX	19-JUL-2001.	
XX	16-JAN-2001; 2001WO-US001651.	
PF	13-JAN-2000; 2000US-0175968P.	
XX	15-MAR-2000; 2000US-00526106.	
PR	15-MAR-2000; 2000US-00526106.	

XX (PANO-) PANORAMA RES INC.
XX
XX Balint RF, Her J;
XX
XX WPI; 2001-451857/48.
XX N-PSDB; AAD10411.
XX
XX Interaction-dependent enzyme association systems for detecting
XX interactions between two or three polypeptides, especially in human
XX therapeutics, diagnostics or prognostics, comprise circularly permuted
XX proteins.
XX
XX Claim 38; Fig 2; 104pp; English.
XX
XX The invention relates to new interaction-dependent enzyme association
XX (IDEA) systems that comprise a fusion sequence that encodes for a
XX circularly permuted, interaction-activated proteins that reassemble to
XX form functionally reconstituted marker proteins which produce a
XX detectable signal upon the association of two oligopeptides, or upon
XX simultaneous association of two oligopeptides with a third oligopeptide.
XX The marker protein is preferably a type A beta-lactamase, especially TEM-
XX 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a
XX proteome library selected from single chain antibody Fv fragment library,
XX an antibody light chain variable region library and a peptide library
XX displayed within thioredoxin. The IDEA systems are useful for detecting
XX and identifying interactions between intracellular as well as
XX extracellular proteins, particularly in selecting with a single marker protein the
XX incorporation of multiple genetic traits in a host cell. In particular,
XX the systems are useful in many applications in human therapeutics,
XX diagnostics and prognostics, as well as in high-throughput screenings
XX systems for the discovery and validation of pharmaceutical targets and
XX drugs. Prior systems (e.g. E. coli Dimer Detection System, Yeast two-
XX hybrid system or Selective Infective Phage System) require multiple steps
XX between interaction and phenotype, which cause severe loss of efficiency
XX due to high false positive and false negative rates. The present system
XX is capable of simultaneous detection of multiple interactions between
XX extra-cellular as well as intracellular proteins in a high throughput
XX format. The circularly permuted marker proteins comprising interaction-
XX dependent enzymes find use in cell-based sensors for activation or
XX inhibition of metabolic or signal transduction pathways, in high-
XX throughput mapping of pair-wise protein-protein interactions within and
XX between the proteomes of cells, tissues and pathogenic organisms, and in
XX cell-based screens for high-throughput selection of inhibitors of any
XX protein-protein interaction. The present sequence is Escherichia coli
XX mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-
XX lactamase is a product of ampicillin resistance gene. The enzyme has two
XX domains, alpha-omega and mu
XX
SQ Sequence 263 AA;
Query Match 100.0%; Score 1032; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQADQGVGYIEIDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
DB 1 HPELVKVKADQADQGVGYIEIDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
QY 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLITTTGGP 120
DB 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLITTTGGP 120
QY 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTTPVAAATTLRKLLTGELLTLASRQ 180
DB 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTTPVAAATTLRKLLTGELLTLASRQ 180
QY 181 QLIDMMEADKVAQPLLSALPA 202
DB 181 QLIDMMEADKVAQPLLSALPA 202
QY 181 QLIDMMEADKVAQPLLSALPA 202
DB 181 QLIDMMEADKVAQPLLSALPA 202

RESULT 2
ID AAB36692
XX AAB36692 standard; protein; 263 AA.
XX
XX AAB36692;
XX
XX 15-MAR-2001 (first entry)
XX
XX Escherichia coli mature TEM-1 beta-lactamase protein sequence.
XX
XX Interaction-activated protein; beta-lactamase; protein interaction.
XX
XX Escherichia coli.
XX
XX WO200071702-A1.
XX
XX 30-NOV-2000.
XX
XX 16-MAR-2000; 2000WO-US007108.
XX
XX 25-MAY-1999; 99US-0135926P.
XX 13-JAN-2000; 2000US-0175968P.
XX
XX (PANO-) PANORAMA RES INC.
XX
XX Balint RF, Her J;
XX
XX WPI; 2001-032034/04.
XX N-PSDB; AAC90773.
XX
XX Novel fragment complementation system to identify interactions between
XX polypeptides comprises fragment pairs having first and second members
XX that reassemble into a marker protein which has a directly detectable
XX signal.
XX
XX Disclosure; Fig 2; 94pp; English.
XX
XX The present invention describes a fragment complementation system (I)
XX which comprises a first oligopeptide (OP1) containing an N-terminal
XX fragment with a C-terminal break point and a second oligopeptide (OP2)
XX comprising a C-terminal with a N-terminal breakpoint, in which the C and
XX N terminal fragments are both derived from a marker protein (MP) and
XX reassemble to form a functionally reconstituted MP. Methods from the
XX present invention are used for monitoring the occurrence of protein-
XX protein interactions in a sample, identifying oligopeptide interactions
XX between two different proteomes, identifying epitopes that bind to an
XX immunoglobulin (Ig) variable region, for identifying interactions between
XX an extracellular domain of a transmembrane protein and a polypeptide, for
XX high-throughput identification of compounds that inhibit phosphorylation-
XX regulated signal transducers, forming a enzyme complementation system for
XX selecting simultaneous incorporation of multiple genetic elements into a
XX host cell and for activating a beta-lactam derivative of an antitumor
XX compound in a host who is in need of it. The present sequence represents
XX the Escherichia coli mature TEM-1 beta-lactamase, which is used in the
XX exemplification of the present invention
XX
SQ Sequence 263 AA;
Query Match 100.0%; Score 1032; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.5e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADQADQGVGYIEIDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
DB 1 HPELVKVKADQADQGVGYIEIDLSGKILSFREPERPMMSTFKVLLCGAVLSRID 60
QY 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLITTTGGP 120
DB 61 AGQQLGRRIHYSONDIVESPVTEKHLTDGMTVRELCSSAATMSDNTAANLLITTTGGP 120
QY 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTTPVAAATTLRKLLTGELLTLASRQ 180
DB 121 KETLAFPLHNMGDHVTRLDRWPEPEINEALPNDERDTTPVAAATTLRKLLTGELLTLASRQ 180

Oy 181 OLIDMEADKVAGPILRSALPA 202
 Db 181 OLIDMEADKVAGPILRSALPA 202

RESULT 3

ID ADJ67709 standard; protein; 263 AA.

AC ADJ67709;

XX 20-MAY-2004 (first entry)

XX Escherichia coli TEM-1 beta-lactamase.

KM fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.

XX Escherichia coli.

XX US2004038317-A1.

XX 26-FEB-2004.

XX 22-SEP-2003; 2003US-00668778.

XX 15-MAR-1999; 99US-0124333P.

XX 25-MAY-1999; 99US-0135926P.

XX 13-JAN-2000; 2000US-0175968P.

XX 15-MAR-2000; 2000US-00526106.

XX (KALO-) KALOBROS INC.

XX Balint RF, Her J;

XX WPI; 2004-203222/19.

XX N-PSDB; ADJ67708.

XX 20-MAY-2004.

XX 22-SEP-2003; 2003US-00668778.

XX 15-MAR-1999; 99US-0124333P.

XX 25-MAY-1999; 99US-0135926P.

XX 13-JAN-2000; 2000US-0175968P.

XX 15-MAR-2000; 2000US-00526106.

XX (KALO-) KALOBROS INC.

XX Balint RF, Her J;

XX WPI; 2004-203222/19.

XX N-PSDB; ADJ67708.

XX 20-MAY-2004.

XX 22-SEP-2003; 2003US-00668778.

XX 15-MAR-1999; 99US-0124333P.

XX 25-MAY-1999; 99US-0135926P.

XX 13-JAN-2000; 2000US-0175968P.

CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.

SQ Sequence 263 AA;

Query Match 100.0%; Score 1032; DB 8; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.5e-103;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HPETLVKVKVADADQAGARVGYIELDNGSKILSESPREPMPMSSTFKVLLCGAVLSRID 60

Db 1 HPETLVKVKVADADQAGARVGYIELDNGSKILSESPREPMPMSSTFKVLLCGAVLSRID 60

Oy 61 AGOGLGRIRIHVSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAAILTTIGCP 120

Db 61 AGOGLGRIRIHVSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAAILTTIGCP 120

Oy 121 KETLAFINMGDHTRLDRWPELNEALPNDERDTTMVAAATTIRKLLTGSELLTLASRO 180

Db 121 KETLAFINMGDHTRLDRWPELNEALPNDERDTTMVAAATTIRKLLTGSELLTLASRO 180

Oy 181 OLIDMEADKVAGPILRSALPA 202

Db 181 OLIDMEADKVAGPILRSALPA 202

RESULT 4

AAW16634

XX AAW16634 standard; protein; 264 AA.

XX AAW16634;

XX 09-AUG-1997 (first entry)

XX DE

XX Beta-lactamase (including signal peptide).

XX KM

XX Gene directed enzyme prodnrg therapy; GDEPT;

XX KM virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;

XX KM HIV; inflammation.

XX OS

XX Escherichia coli.

XX FH

XX Key

XX Peptide

XX 1.23

XX /label= sig_peptide

XX MO9719180-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002845.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAX) GLAXO GROUP LTD.

XX Dev I, Moore JT, Ohmstede C;

XX WPI; 1997-298117/27.

XX N-PSDB; AAW16634.

XX Molecular chimera for gene or virus directed enzyme prodnrg therapy -

XX useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 28; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16634), including the signal peptide,

XX is the expression product of a molecular chimera, designated PCMV-BL

XX (AAW16634), in which the beta-lactamase gene is under control of the CMV

XX intermediate/early promoter. Vectors consisting of a transcriptional

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CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a prodrug into an agent toxic to the cell for
 CC treatment of cancer. viral. (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 1032; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 1.5e-103; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADDDGARGVYIEIDLSNGKILLESFRRPFRPMMSTFVLLCGAVLSRID 60

DB 2 HPELVKVKDADDDGARGVYIEIDLSNGKILLESFRRPFRPMMSTFVLLCGAVLSRID 61

QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 120

DB 62 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 121

QY 121 KELTAFLLNMGDHYTRLDRWEPBELNEAIPNDRDITMPVMAATTLRKLLTGELLTLASRQ 180

DB 122 KELTAFLLNMGDHYTRLDRWEPBELNEAIPNDRDITMPVMAATTLRKLLTGELLTLASRQ 181

QY 181 QLIDMMEADKVAGPLRSALPA 202

DB 182 QLIDMMEADKVAGPLRSALPA 203

RESULT 5
 AAW18680
 ID AAW18680 standard; protein; 264 AA.

XX AAW18680;

XX 13-AUG-1997 (first entry)

XX Intracellularly-expressed beta-lactamase.

XX Producing therapy; gene directed enzyme producing therapy; GDBPT;

XX Virus directed enzyme producing therapy; VDEPT; lung cancer;

XX beta-lactamase; PCMV-delBL.

XX Escherichia coli.

XX W09719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAXO) GLAXO GROUP LTD.

XX Dev I, Moore JT, Setluna PB;

XX WPI; 1997-298118/27.

XX N-PSDB; AAT70311.

XX DNA construct for gene-directed enzyme producing therapy of lung cancer -

XX comprises lung- or neuroendocrine-specific promoter controlling

XX expression of producing-converting enzyme.

XX Example 811; Page 32-34; 53pp; English.

XX The intracellular form (AAW18680) of TEM beta-lactamase is expressed by
 CC PCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding
 CC sequence, minus the signal sequence, is placed under control of the
 CC intermediate/early promoter of cytomegalovirus. Intracellular beta-
 CC lactamase constructs, placed under control of promoter/enhancer elements
 CC of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in producing therapy of lung
 CC cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 1032; DB 2; Length 264;

Best Local Similarity 100.0%; Pred. No. 1.5e-103; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKDADDDGARGVYIEIDLSNGKILLESFRRPFRPMMSTFVLLCGAVLSRID 60

DB 2 HPELVKVKDADDDGARGVYIEIDLSNGKILLESFRRPFRPMMSTFVLLCGAVLSRID 61

QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 120

DB 62 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGCP 121

QY 121 KELTAFLLNMGDHYTRLDRWEPBELNEAIPNDRDITMPVMAATTLRKLLTGELLTLASRQ 180

DB 122 KELTAFLLNMGDHYTRLDRWEPBELNEAIPNDRDITMPVMAATTLRKLLTGELLTLASRQ 181

QY 181 QLIDMMEADKVAGPLRSALPA 202

DB 182 QLIDMMEADKVAGPLRSALPA 203

RESULT 6
 AAR31575
 ID AAR31575 standard; protein; 286 AA.

XX AAR31575;

XX 10-MAR-2003 (revised)

XX 04-JUN-1993 (first entry)

XX Ampicillin resistance protein.

XX CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

XX xenobiotics; circular; chimeric cytochrome P4501A1.

XX Homo sapiens.

XX US5180666-A.

XX 19-JAN-1993.

XX 27-JUN-1991; 91US-00721775.

XX 27-JUN-1991; 91US-00721775.

XX (UYWA-) UNIV WAYNE STATE.

XX States JC, Hines RM, Novak RF;

XX WPI; 1993-052845/06.

XX N-PSDB; AAQ36498.

XX In vitro method for testing mutagenicity of a chemical - by metabolising

XX chemical cell line consisting of transformed fibroblasts having

XX detectable cytochrome P450 mixed function oxidase activity and detecting

XX gene damage.

XX Disclosure; Col 21-24; 24pp; English.

XX The expression constructs PRNH127 and PRNH155 contain identical sequences
 CC but were constructed using different strategies (see AAQ36498). The
 CC constructs comprise exons 2-7 of human CYP1A1 gene under the control of
 CC the inducible mouse metallothionein (MT-1) promoter. The constructs also
 CC contain an open reading frame in the opposite orientation to the
 CC cytochrome P450 exons. This ORF encodes ampicillin resistance. The
 CC constructs are suitable for transformation of human fibroblasts derived
 CC from the xeroderma pigmentosum group A. Cultures of the transformed
 CC fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
 CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
 CC field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDINSKILIESFRPEERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKXVDADQAGARVGYIELDINSKILIESFRPEERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLDGNTVRELCSAATMDSNTANILLTTIGSP 120
 DB 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLDGNTVRELCSAATMDSNTANILLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTPVAMATTIRKLLTGELITLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTPVAMATTIRKLLTGELITLASRQ 203
 QY 181 QLIDWMEADKVAAGPILRSALPA 202
 DB 204 QLIDWMEADKVAAGPILRSALPA 225

RESULT 7

AAR97619 AAR97619 standard; protein; 286 AA.

XX AAR97619;

DT 20-AUG-1996 (first entry)

XX Secretory beta-lactamase.

DE Gene therapy; gene directed enzyme prodng therapy; GDEPT;

KM virus directed enzyme prodng therapy; VDEPT; prodng activation;

KW cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;

KV beta-lactamase; cephalosporin.

XX Synthetic.

OS MO6616179-A1.

XX 30-MAY-1996.

PD 20-NOV-1995; 95WO-GB002716.

XX 18-NOV-1994; 94GB-00023367.

PR (WBL) WBLCOMB FOUND LTD.

XX Dev IK, Moore JT, Ohmstede C;

PI WPI; 1996-268615/27.

DR N-PSDB; AAT29220.

XX Molecular chimera for use in enzyme gene therapy - is activated in a

PT target cell to express a secretible enzyme which cleaves a prodng

PT outside the cell into a cytotoxic or cytostatic agent.

XX Example 3; Page 57-58; 73pp; English.

PS A secretory beta-lactamase (AAR97619) is expressed from DNA construct

CC PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under

CC the control of the intermediate/early cytomagalovirus promoter. Beta-

CC lactamase delivery to mammalian cells confers sensitivity to

CC cephalosporin prodngs. Liposomal DNA/5-fluorouracil prodng combinations

CC resulted in 8.c. tumour regression in mice bearing A549 tumours. Survival

CC of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours

CC was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct

XX Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXVDADQAGARVGYIELDINSKILIESFRPEERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPEITLVKXVDADQAGARVGYIELDINSKILIESFRPEERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLDGNTVRELCSAATMDSNTANILLTTIGSP 120
 DB 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLDGNTVRELCSAATMDSNTANILLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTPVAMATTIRKLLTGELITLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDPTTPVAMATTIRKLLTGELITLASRQ 203
 QY 181 QLIDWMEADKVAAGPILRSALPA 202
 DB 204 QLIDWMEADKVAAGPILRSALPA 225

RESULT 8

AAR96423 AAR96423 standard; protein; 286 AA.

XX AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

XX Cytochrome P450 (CYP1A1 construct).

KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

KW metabolism.

XX Homo sapiens.

OS US5525482-A.

XX 11-JUN-1996.

PD 15-NOV-1994; 94US-00339658.

XX 27-JUN-1991; 91US-00721775.

PR 09-DEC-1992; 92US-00990295.

XX (UYWA-) UNIV WAYNE STATE.

XX Hines RN, Novak RF, States JC;

PI WPI; 1996-286397/29.

DR N-PSDB; AAT30354.

XX Testing chemicals for cytotoxicity to human by detecting gene damage -

PT using recombinant fibroblasts transformed with cytochrome P450 gene under

PT control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

PS The present sequence is encoded by a chimeric mouse metallothionein-

CC cytochrome P4501A1 (CYP1A1) expression construct. Two clones, pRNH127 and

CC pRNH15, were isolated by different methods and which both had the same

CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity

CC of humans to a chemical. The method comprises exposing human fibroblast

CC cells normally not including any cytochrome P450 activity to potentially

CC toxic chemicals. The cells having been transformed to express cytochrome

CC P450, under the control of a controllable promoter through the CYP1A1

CC gene, upon exposure to the chemical in vitro. The chemical is metabolised

CC intracellularly into a cytochrome metabolite by oxidation within the

CC fibroblasts through the intracellular cytochrome P450 mixed function
CC oxidase enzymes expressed by the cells. Gene damage in the test cells is
CC detected as an indication of cytotoxicity of the chemical. (Updated on 25
CC -MAR-2003 to correct PF field.)

SQ Sequence 286 AA;

Query Match	100.0%	Score 1032	DB 2	length 286
Best Local Similarity	100.0%	Pred. No. 1.7e-103		
Matches 202; Conservative	0	Mismatches	0	Gaps - 0

[illegible]

RESULT 9
AAW16635

AC AAW16635;

DT 09-AUG-1997 (first entry)

Beta-Lactamase (no signal peptide) :

KM Gene directed enzyme product therapy; GDEPT;
KM virus directed enzyme product therapy; VDEPT; beta-lactamase; cancer;
KM HIV; inflammation.

OS *Escherichia coli*.

PN W09719180-A2.
yy

PD 29-MAY-1997.
XX

13-NOV-1990, 2000-080020430

xx

PA (GLAX) GLAXO GROUP LTD.

Dev I, Moore JT, Ohmstede C,
PI
xx

DR WPL: 1997-29811/21.
DR N-PSNB: AAT66737.

PT Molecular chimae

PT Molecular chaperone for gene or virus directed enzyme prodrug therapy -
PT useful for treatment of cancer, viral infection or inflammation.
XX

PS Example; Page 26; 38pp; English.

CC Escherichia coli beta-lactamase (AAM16635), lacking the signal peptide,
CC is the expression product of a molecular chimera, designated pCMV-deltaB,
CC (AAM66738), in which the beta-lactamase gene is under control of the CMV
CC intermediate/early promoter. Vectors consisting of a transcriptional
CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
CC enzyme producing therapy. Intracellular expression of the beta-lactamase in
CC a targeted cell allows conversion of a prodrug into an agent toxic to
CC the cell for treatment of cancer, viral (e.g. HIV) infection or
CC inflammation

XX Sequence 286 AA;
SQ

Query Match	100.0%	Score 1032	DB 21	Length 286
Best Local Similarity	100.0%	Pred. No. 1.7e-103		
Matches 202	0	Mismatches	0	Gaps 0

Qy	1	HEPTLVKVDABEOLGARGVYIELDNSGKILIESRPERPMMSTFVLLCGAVLSRID	60
Db	24	HEPTLVKVDABEOLGARGVYIELDNSGKILIESRPERPMMSTFVLLCGAVLSRID	83
Qy	61	AGGEOIGARRIHYSONDLVEYSPVTEKHLTDGNTVYELCSAIIYMSDNTAANLLFTTIGP	120
Db	84	AGGEOIGARRIHYSONDLVEYSPVTEKHLTDGNTVYELCSAIIYMSDNTAANLLFTTIGP	143
Qy	121	KEITATLHNMGGHVTRLDRMEPELNEAIPNDERDPTTMYVAAATTLRKLITGELLTLASRQ	180
Db	144	KEITATLHNMGGHVTRLDRMEPELNEAIPNDERDPTTMYVAAATTLRKLITGELLTLASRQ	203
Qy	181	QLIDMMEADKVAAGPTLRSALPA	202
Db	204	QLIDMMEADKVAAGPTLRSALPA	225

RESULT 10
AAW18679
ID AAW18679 standard; protein; 286 AA.

AC AA18679;
VY

DT 13-AUG-1997 (first entry)
XX

XX DECEMBER 1964-1965

KW prodnug therapy; gene directed enzyme prodnug therapy; GDEPT
 KW virus directed enzyme prodnug therapy; VDEPT; lung cancer;
 beta-lactamase; pCMV-BL.
 XX

OS Escherichia coli.
Y

FT	Penitide	Location/Qualifiers
EH	Key	1-23

Protein	/label= sig_peptide
FT	34 386
EM	

FT /label= Mat_protein

PN WO9719183-A2.

PD 29-MAY-1997
XX

19-NOV-1996; 38MC-GB002846.

[illegible]PA (GLAX) GLAXO GROUP LTD.
XX
XX

XX
F1 DEV 1, MOORE 01, SECURIDA FB/

DR N-PSDB; AAT70309.

PT	DNA construct for
1	1
2	2
3	3
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5	5
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89	89
90	90
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97	97
98	98
99	99
100	100

PT expression of prodrug-converting enzyme.

Example 811; Page 26-27; 53pp; English.

CC The selected form (AAAT18679) of TEM beta-lactamase is expressed by pCMV-
CC BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is
CC placed under control of the intermediate/early promoter of
CC cytomegalovirus. Secretary beta-lactamase constructs, placed under
CC control of promoter/enhancer elements of lung-associated protein or
CC neuroendocrine marker protein genes, can be used in novel chimaeric

CC molecules for use in prodrg therapy of lung cancer
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGVGYIELDNSGKILSPRPERPFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGVGYIELDNSGKILSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELTLTASRQ 180
DB 144 KELTAFILNMGDHYRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELTLTASRQ 203
QY 181 OLIDWMEADKVAAGPILRSALPA 202
DB 204 OLIDWMEADKVAAGPILRSALPA 225
RESULT 11
AA08529
ID AA08529 standard; protein; 286 AA.
AC AA08529;
XX
XX 03-AUG-1999 (first entry)
DT
XX Vector pASK75 beta-1a protein.
DE
XX Firefly; luciferase; tetracycline; transcriptional control; Tetr; Teta;
KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
KW allergy.
XX
XX Synthetic.
OS
XX MO9925866-A1.
PN
XX 27-MAY-1999.
PD
XX 11-NOV-1998; 98WO-FI000873.
PF
XX 14-NOV-1997; 97FI-00004235.
PR
XX (KORP/) KORBELA M.
PA (KARP/) KARP M.
PA (KURI/) KURITU J.
XX
PI Korpela M, Karp M, Kuritu J;
XX
XX WPI; 1999-338015/28.
DR N-PSDB; AAV72418.
DR
XX
XX Assaying for tetracycline using recombinant prokaryotic cells.
PT
XX
XX Disclosure; Page 47-48; 67pp; English.
PS
XX This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline from other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxCDABE
CC genes, a tetracycline repressor (Tetr) and a tetracycline promoter (Teta)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (Tetr)
CC and a tetracycline promoter (Teta) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,

CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected
XX
XX Sequence 286 AA;
SQ
Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGVGYIELDNSGKILSPRPERPFPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKVDADQAGVGYIELDNSGKILSPRPERPFPMSTFKVLLCGAVLSRID 83
QY 61 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGOEOLGRRIRHSQNDLVEYSPVTEKHLTDGVTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KELTAFILNMGDHYRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELTLTASRQ 180
DB 144 KELTAFILNMGDHYRLDRWEPBELNEAIPNDRDITMPVAAATTIRKLLTGELTLTASRQ 203
QY 181 OLIDWMEADKVAAGPILRSALPA 202
DB 204 OLIDWMEADKVAAGPILRSALPA 225
RESULT 12
AAB10442
ID AAB10442 standard; protein; 286 AA.
AC AAB10442;
XX
XX 01-DEC-2000 (first entry)
DT
XX Expression vector pSEX15G2 bla protein.
DE
XX
XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
KW
XX
XX Synthetic.
OS
XX DE19900635-A1.
PN
XX 13-JUL-2000.
PD
XX 11-JAN-1999; 99DE-01000635.
PF
XX 11-JAN-1999; 99DE-01000635.
PR
XX (DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.
PA
XX Breilting F, Pouscka A, Moldenhauer G;
XX
XX WPI; 2000-499832/45.
DR N-PSDB; AAV71430.
DR
XX
XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.
PT
XX
XX Claim 16; Fig 3; 22pp; German.
PS
XX This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The

CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD53. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX114 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSGKILSPFRPERFPMWSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSPFRPERFPMWSTFKVLLCGAVLSRID 83
QY 61 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGSP 120
DB 84 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGSP 143
QY 121 KEITAFILNMGDHTRLDKRWPELNEAIPNDERDTVMVAATTIRKLLTGEILTLASRQ 180
DB 144 KEITAFILNMGDHTRLDKRWPELNEAIPNDERDTVMVAATTIRKLLTGEILTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSLALPA 202
DB 204 QLIDWMEADKVAGPLLRSLALPA 225

RESULT 13
AAB10438
ID AAB10438 standard; protein; 286 AA.

XX AC AAB10438;
XX DT 01-DEC-2000 (first entry)
XX DE Expression vector pSEX114 bla protein.
XX KM Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX OS Synthetic.
XX PN DE19900635-A1.
XX PD 13-JUL-2000.
XX PF 11-JAN-1999; 99DE-01000635.
XX PR 11-JAN-1999; 99DE-01000635.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Breitling F, Poustka A, Moldenhauer G;
XX MPI; 2000-499832/45.
XX DR N-PSDB; AAA71428.
XX Selecting monoclonal antibodies, by expressing them on the surface of
XX hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.
XX Claim 16; Fig 1; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (I) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD53. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the Neo-R
CC protein contained in the expression vector pSEX114 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-103;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSGKILSPFRPERFPMWSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSPFRPERFPMWSTFKVLLCGAVLSRID 83
QY 61 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGSP 120
DB 84 AGQSGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITWSDNTAANLLTTIGSP 143
QY 121 KEITAFILNMGDHTRLDKRWPELNEAIPNDERDTVMVAATTIRKLLTGEILTLASRQ 180
DB 144 KEITAFILNMGDHTRLDKRWPELNEAIPNDERDTVMVAATTIRKLLTGEILTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSLALPA 202
DB 204 QLIDWMEADKVAGPLLRSLALPA 225

RESULT 14
AAB10440
ID AAB10440 standard; protein; 286 AA.

XX AC AAB10440;
XX DT 01-DEC-2000 (first entry)
XX DE Expression vector pSEX112 bla protein.
XX KM Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
XX B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
XX OS Synthetic.
XX PN DE19900635-A1.
XX PD 13-JUL-2000.
XX PF 11-JAN-1999; 99DE-01000635.
XX PR 11-JAN-1999; 99DE-01000635.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Breitling F, Poustka A, Moldenhauer G;
XX MPI; 2000-499832/45.
XX DR N-PSDB; AAA71429.
XX Selecting monoclonal antibodies, by expressing them on the surface of

PT hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.

PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, I or Ig, and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX10g which contains the
CC bla protein. Neo-R and protein G described in the method of the invention
XX

SQ Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQUGARVGYIELDLSGKILSFRRPFRPMSFTFKVLCGAVLSRID 60
DB 24 HPEITLVKVDADQUGARVGYIELDLSGKILSFRRPFRPMSFTFKVLCGAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTANLLTTIGGP 120
DB 84 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELTAFLEHMGDHTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 180
DB 144 KELTAFLEHMGDHTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
DB 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 15

AAB50898 ID AAB50898 standard; protein; 286 AA.

XX AAB50898;

XX 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

XX bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; cel2 gene;
KW glucanase; integration vector; pLO12306.

XX Unidentified.

XX WO200071729-A2.

XX 30-NOV-2000.

XX 26-MAY-2000; 2000MO-US014773.

XX 26-MAY-1999; 99US-0136376F.

XX (UYFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;
XX
XX MPI; 2001-032043/04.
DR N-PSDB; AAC91455.

XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.
PS Disclosure; Page 82-83; 87pp; English.

XX The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the cel2 gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence
XX

SQ Sequence 286 AA;

Query Match 100.0%; Score 1032; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.7e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQUGARVGYIELDLSGKILSFRRPFRPMSFTFKVLCGAVLSRID 60
DB 24 HPEITLVKVDADQUGARVGYIELDLSGKILSFRRPFRPMSFTFKVLCGAVLSRID 83
QY 61 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTANLLTTIGGP 120
DB 84 AGQEQLGRRIRHSQNDLVEYSPVTEKHLLTDGNTVRELCSAATMSDNTANLLTTIGGP 143
QY 121 KELTAFLEHMGDHTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 180
DB 144 KELTAFLEHMGDHTRLDRWPELNEALPNDERDITMPVAMATTIRKLLTGELTLTASRQ 203
QY 181 QLIDWMEADKVAAGPLRSALPA 202
DB 204 QLIDWMEADKVAAGPLRSALPA 225

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Job time : 79.3206 secs

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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:36:31 ; Search time 20.7105 Seconds
(without alignments)
728.091 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202

Perfect score: 1032
Sequence: 1 HPEITLVKVKADMDQIGARVG.....IDWMEADRVAGPLRSALPA 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1032	100.0	286	1	US-07-721-775A-2
2	1032	100.0	286	1	US-08-339-658-2
3	1032	100.0	286	3	US-09-263-933-7
4	1032	100.0	286	3	US-09-263-933-14
5	1032	100.0	286	3	US-09-263-933-21
6	1032	100.0	286	3	US-09-025-769B-265
7	1032	100.0	286	3	US-09-025-769B-362
8	1032	100.0	286	4	US-09-919-901-7
9	1032	100.0	286	4	US-09-919-901-14
10	1032	100.0	286	4	US-09-919-901-21
11	1032	100.0	286	4	US-09-490-070A-265
12	1032	100.0	286	4	US-09-490-070A-362
13	1032	100.0	286	4	US-09-490-153-265
14	1032	100.0	286	4	US-09-490-153-362
15	1032	100.0	286	4	US-10-191-966-7
16	1032	100.0	286	4	US-10-191-966-14
17	1032	100.0	286	4	US-10-191-966-21
18	1032	100.0	286	4	US-09-490-324-265
19	1032	100.0	286	4	US-09-490-324-362
20	1032	100.0	286	3	US-09-025-769B-285
21	1032	100.0	286	3	US-09-025-769B-298
22	1032	100.0	286	3	US-09-025-769B-300
23	1032	100.0	286	4	US-09-490-070A-285
24	1032	100.0	286	4	US-09-490-070A-298
25	1032	100.0	286	4	US-09-490-070A-300
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27	1032	100.0	286	4	US-09-490-153-298

28	1032	100.0	299	4	US-09-490-153-300	Sequence 300, App
29	1032	100.0	299	4	US-09-490-324-285	Sequence 285, App
30	1032	100.0	299	4	US-09-490-324-298	Sequence 298, App
31	1032	100.0	299	4	US-09-490-324-300	Sequence 300, App
32	1032	100.0	299	3	US-09-263-933-2	Sequence 2, Appl1
33	1032	100.0	299	3	US-09-263-933-9	Sequence 9, Appl1
34	1032	100.0	299	3	US-09-263-933-16	Sequence 16, Appl1
35	1032	100.0	299	4	US-09-919-901-2	Sequence 2, Appl1
36	1032	100.0	299	4	US-09-919-901-9	Sequence 9, Appl1
37	1032	100.0	299	4	US-09-919-901-16	Sequence 16, Appl1
38	1032	100.0	299	4	US-10-191-966-2	Sequence 2, Appl1
39	1032	100.0	299	4	US-10-191-966-9	Sequence 9, Appl1
40	1032	100.0	299	4	US-10-191-966-16	Sequence 16, Appl1
41	1031	99.9	286	4	US-09-555-510B-9	Sequence 9, Appl1
42	1031	99.9	286	4	US-10-231-013-9	Sequence 9, Appl1
43	1031	99.9	1293	4	US-09-170-466D-292	Sequence 292, App
44	1031	99.9	1293	4	US-09-364-425B-57	Sequence 57, Appl1
45	1027	99.5	263	1	US-08-407-544-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-721-775A-2
Sequence 2, Application US/07721775A
Patent No. 5180666
GENERAL INFORMATION:
APPLICANT: States, J. Christopher
APPLICANT: Hines, Ronald N.
APPLICANT: No. 5180666ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSER: Relating, Echington, Barnard, Perry & Milton
STREET: P. O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07721, 775A
FILING DATE: 19910627
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30, 955
REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEFAX: (313) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-721-775A-2

Query Match 100.0%; Score 1032; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADMDQIGARVGIETDINSKILSEPRPPEPMMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADMDQIGARVGIETDINSKILSEPRPPEPMMSTFVLLCGAVLSRID 83

Qy	61	AGOEGLGRIRHXSQNDLVEYSPVTEBHLTDGVTRELSGPAALITMSQNTANLLTTIGG	120
Db	84	AGOEGLGRIRHXSQNDLVEYSPVTEBHLTDGVTRELSGPAALITMSQNTANLLTTIGG	143
Qy	121	KELTPFLNNMGDHYRLDRMBEPLNEALPNDSDRDTTPYAMATTLAKLTGELLTTASRQ	180
Db	144	KELTPFLNNMGDHYRLDRMBEPLNEALPNDSDRDTTPYAMATTLKRLNGELLTLASRQ	203
Qy	181	QLIDWMEADKVAAGELLRSALPA	202
Db	204	QLIDWMEADKVAAGELLRSALPA	225

RESULT 2
 US-08-339-658-2
 Sequence 2, Application US/068339658
 Patent No. 5525482
 GENERAL INFORMATION:
 APPLICANT: States, J. Christopher
 APPLICANT: Hines, Ronald N.
 APPLICANT: No. 5525482ak, Raymond F.
 TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
 NUMBER OF INVENTION: MUTAGENICITY OF A CHEMICAL
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Raisting, Ethington, Barnard, Perry & Milton
 STREET: P.O. Box 4390
 CITY: Troy
 STATE: Michigan
 COUNTRY: U.S.A.
 ZIP: 48099
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentm Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/339,658
 FILING DATE: 15-NOV-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/990,295
 FILING DATE: 09-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30,955
 REFERENCE/DOCKET NUMBER: P-321MSU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (313) 689-3554
 TELEFAX: (313) 689-4071
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 286 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-339-658-2

Query Match	100.0%	Score 1032;	DB 1;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 1.6e-113;		
Matches 202; Conservative	0;	Mismatches	0;	Indels 0

Qy	1	HPETLVKQKADBDQCGARVGYIELDLSKILIESFPERPFPMMSTFKYLLCGAVLSRID	60
Db	24	HPETLVKQKADBDQCGARVGYIELDLSKILIESFPERPFPMMSTFKYLLCGAVLSRID	83
Qy	61	AGQGLGRIRHYSQNDLVEYSPYTEKHLIDMGTVIELCSAALTMSQNTAAILLTITIGSP	120
Db	84	AGQGLGRIRHYSQNDLVEYSPYTEKHLIDMGTVIELCSAALTMSQNTAAILLTITIGSP	143
Qy	121	KELTALFLHNMGDHVTLRDMEPELNEALPNDERSDDTTPVAAATTLKLLTGBLILTASQ	180
Db	144	KELTALFLHNMGDHVTLRDMEPELNEALPNDERSDDTTPVAAATTLKLLTGBLILTASQ	203

QY	181	QLIDMMEADKVAGPLLRSA	LP	202
Db	204	QLIDMMEADKVAGPLLRSA	LP	225

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RESULT 3
US-09-263-933-7
Sequence 7, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OR INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-06
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial Sequence
US-09-263-933-7

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Query Match	100.0%;	Score 1032;	DB 3;	Length 286;
Best Local Similarity	100.0%;	Pred. No. 1.6e-113;		
Matches	202;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
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Db	24	HPETLVYKQKAEQDQARVGTYIEDLNSGKLTLESRRPFRPPMSTFKVLLCGAVLSRD	83	
Qy	61	AGQEGGRIRIHYSONDVAEYSPTEKHLTDGMYELCSAIIYMSDNTAANLLTTIGSP	120	
Db	84	AGQEGGRIRIHYSONDVAEYSPTEKHLTDGMYRELCSAIIYMSDNTAANLLTTIGSP	143	
Qy	121	KELTAFLHNMGDVATRLDRWEPELNEALPNDERDITPMVAMATYLRKLITGELLTLASRQ	180	
Db	144	KELTAFLHNMGDVATRLDRWEPELNEALPNDERDITPMVAMATYLRKLITGELLTLASRQ	203	
Qy	181	QIDMMEADKVAGPLLSALPA	202	
Db	204	QIDMMEADKVAGPLLSALPA	225	

```

RESULT 4
US-09-263-933-14
, Sequence 14: Application US/09263933
, Patent No. 6280940
, GENERAL INFORMATION:
, APPLICANT: Potts, Karen E.
, APPLICANT: Jackson, Roberta L.
, APPLICANT: Patrick, Amy K.
, TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
, TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
, FILE REFERENCE: 0125-0005A
, CURRENT APPLICATION NUMBER: US/09/263,933
, CURRENT FILING DATE: 1999-03-08
, EARLIER APPLICATION NUMBER: 09/129,611
, EARLIER FILING DATE: 1998-08-05
, NUMBER OF SEQ ID NOS: 33
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 14
, LENGTH: 286
, TYPE: PRT
, ORGANISM: Artificial Sequence
, US-09-263-933-14

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Query Match 100.0%; Score 1032; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.6e-113;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDNSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADADQAGRVGYIELDNSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KETLTFILNMGDHYTRLDRWBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KETLTFILNMGDHYTRLDRWBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 QLIDWMEADKVAAGPLRSALPA 202
 DB 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 5

US-09-263-933-21
 ; Sequence 21, Application US/09263933
 ; Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potte, Karen E.
 APPLICANT: Jackson, Roberta L.
 APPLICANT: Patrick, Amy K.
 TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
 FILE REFERENCE: 0125-0005A
 CURRENT APPLICATION NUMBER: US/09/263, 933
 CURRENT FILING DATE: 1999-03-08
 EARLIER APPLICATION NUMBER: 09/129, 611
 EARLIER FILING DATE: 1998-08-05
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 21
 LENGTH: 286
 TYPE: PRT
 ORGANISM: Artificial Sequence
 US-09-263-933-21

Query Match 100.0%; Score 1032; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.6e-113;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDNSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADADQAGRVGYIELDNSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KETLTFILNMGDHYTRLDRWBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KETLTFILNMGDHYTRLDRWBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 QLIDWMEADKVAAGPLRSALPA 202
 DB 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 6

US-09-025-769B-265
 ; Sequence 265, Application US/09025769B
 ; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: MORPHO/5
 INFORMATION FOR SEQ ID NO: 265:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 286 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE:

protein
 US-09-025-769B-265

Query Match 100.0%; Score 1032; DB 3; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.6e-113;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDNSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 60
 DB 24 HPELVKVKADADQAGRVGYIELDNSGKILSFPRPERPFPMSTFKVLLCGAVLSRID 83
 QY 61 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQEQGRIRIHVSQNDLVEYSPVTEKHLTDGVTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KETLTFILNMGDHYTRLDRWBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 180
 DB 144 KETLTFILNMGDHYTRLDRWBEPLNEALPNDERDITTPVAAATTIRKLLTGELLTLASRQ 203
 QY 181 QLIDWMEADKVAAGPLRSALPA 202
 DB 204 QLIDWMEADKVAAGPLRSALPA 225

RESULT 7

US-09-025-769B-362
 ; Sequence 362, Application US/09025769B
 ; Patent No. 6300064

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: Ilag, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-362

Query Match 100.0%; Score 1032; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPREPRPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPREPRPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 120
DB 84 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 143
QY 121 KETAFILNMGDHTRLDRWEPELNEAIPNDEPDTMPVNAATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHTRLDRWEPELNEAIPNDEPDTMPVNAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDMEADKVAGPLRSALPA 202
DB 204 QIIDMEADKVAGPLRSALPA 225

RESULT 8
US-09-919-901-7
Sequence 7, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7

LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-7

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPREPRPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPREPRPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 120
DB 84 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 143
QY 121 KETAFILNMGDHTRLDRWEPELNEAIPNDEPDTMPVNAATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHTRLDRWEPELNEAIPNDEPDTMPVNAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDMEADKVAGPLRSALPA 202
DB 204 QIIDMEADKVAGPLRSALPA 225

RESULT 9
US-09-919-901-14
Sequence 14, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:
US-09-919-901-14

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPREPRPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKKVKAEDDQAGRVGTYIEDLNSGKILBSFRPREPRPMSTFVLLCGAVLSRID 83
QY 61 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 120
DB 84 AGGOLGRRHYSONDLVEYSPVTEKHLTDGMYRELCSAITSNDTNAULLTTIGCP 143
QY 121 KETAFILNMGDHTRLDRWEPELNEAIPNDEPDTMPVNAATTLRKLLTGELLTLASRQ 180
DB 144 KETAFILNMGDHTRLDRWEPELNEAIPNDEPDTMPVNAATTLRKLLTGELLTLASRQ 203
QY 181 QIIDMEADKVAGPLRSALPA 202

Db 204 QUIDMEADKVAAGPLRSALPA 225

RESULT 10

US-09-919-901-21

Sequence 21, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:

APPLICANT: Potte, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patrick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 286

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION:

US-09-919-901-21

Query Match 100.0%; Score 1032; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.6e-113;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSNGKILIESFRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGAVGYIELDLSNGKILIESFRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGGP 120
DB 84 AGQELGRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGGP 143
QY 121 KETLFLNMGDHYTRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGSLTLASRQ 180
DB 144 KETLFLNMGDHYTRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGSLTLASRQ 203
QY 181 QUIDMEADKVAAGPLRSALPA 202
DB 204 QUIDMEADKVAAGPLRSALPA 225

RESULT 11

US-09-490-070A-265

Sequence 265, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McLaughlin

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 100.0%; Score 1032; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 1.6e-113;

Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGAVGYIELDLSNGKILIESFRPERFPMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADADQAGAVGYIELDLSNGKILIESFRPERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQELGRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGGP 120
DB 84 AGQELGRIHYSONDLVEYSPVTEKHLTDGNTVRELCSAAITMSDNTAANLLTTIGGP 143
QY 121 KETLFLNMGDHYTRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGSLTLASRQ 180
DB 144 KETLFLNMGDHYTRLDRWPELNEALPNDERDTTTPVAAATTIRKLLTGSLTLASRQ 203
QY 181 QUIDMEADKVAAGPLRSALPA 202
DB 204 QUIDMEADKVAAGPLRSALPA 225

RESULT 12

US-09-490-070A-362

Sequence 362, Application US/09490070A

Patent No. 6696248

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McLaughlin

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQIGARVGYIELDINSKILBSFRPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQIGARVGYIELDINSKILBSFRPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGCP 120
DB 84 AGQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGCP 143
QY 121 KETLAFPHNMGDHVTLRDWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFPHNMGDHVTLRDWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMEADKVAGPLRSALPA 202
DB 204 QLIDMEADKVAGPLRSALPA 225

RESULT 13
US-09-490-153-265
Sequence 265, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-153-265

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113; Indels 0; Gaps 0;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKKAEDQIGARVGYIELDINSKILBSFRPERPPMSTFKVLLCGAVLSRID 60
DB 24 HPEITLVKKAEDQIGARVGYIELDINSKILBSFRPERPPMSTFKVLLCGAVLSRID 83
QY 61 AGQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGCP 120
DB 84 AGQOLGRRIRHSQNDLVEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANLLTTIGCP 143
QY 121 KETLAFPHNMGDHVTLRDWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KETLAFPHNMGDHVTLRDWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDMEADKVAGPLRSALPA 202
DB 204 QLIDMEADKVAGPLRSALPA 225

RESULT 14
US-09-490-153-362
Sequence 362, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 362:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-153-362

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KeltaFLHNMGDHVTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHNMGDHVTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIDMEADKVAGPILRSALPA 202
DB 204 QLIIDMEADKVAGPILRSALPA 225

RESULT 15

US-10-191-966-7
Sequence 7, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potte, Karen B.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIOR FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-7

Query Match 100.0%; Score 1032; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 60
DB 24 HPEITLVKTKDAEDQIGARVGYIELDLSGKILSFPRPERFPMSTFKYLICGAVLSRID 83
QY 61 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120

DB 84 AGQEQIGRRIRHSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143
QY 121 KeltaFLHNMGDHVTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KeltaFLHNMGDHVTRLDRWEPBELNEAIPNDERDTTMAPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIIDMEADKVAGPILRSALPA 202
DB 204 QLIIDMEADKVAGPILRSALPA 225

Search completed: June 10, 2005, 11:01:17
Job time : 21.7105 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 67.6736 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_202
Perfect score: 1032
Sequence: 1 HPELVKVKDABDQAGARVG.....IDWMEADKVAAGPLRSALPA 202

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_tramb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1032	100.0	229	2	06W9J1 enterobacte
2	1032	100.0	231	2	06W9J2 zymomonas m
3	1032	100.0	241	2	06W9J3 acinetobact
4	1032	100.0	242	2	06W9J4 citrobacter
5	1032	100.0	285	2	06W9J5 klebsiella
6	1032	100.0	286	2	06W9J6 shigella fl
7	1032	100.0	286	2	06W9J7 neisseria m
8	1032	100.0	286	2	06W9J8 salmonella
9	1032	100.0	286	2	06W9J9 serratia ma
10	1032	99.5	225	2	06W9J10 enterobacte
11	1027	99.5	232	2	06W9J11 enterobacte
12	1027	99.5	255	2	06W9J12 enterobacte
13	1027	99.5	261	2	06W9J13 enterobacte
14	1027	99.5	264	2	06W9J14 enterobacte
15	1027	99.5	281	2	06W9J15 enterobacte
16	1027	99.5	282	2	06W9J16 enterobacte
17	1027	99.5	286	1	BLAT_ECOLI
18	1027	99.5	286	1	BLAT_SALTI
19	1027	99.5	286	2	053043
20	1027	99.5	286	2	06W9J17 enterobacte
21	1027	99.5	286	2	06W9J18 enterobacte
22	1027	99.5	286	2	06W9J19 enterobacte
23	1027	99.5	286	2	06W9J20 enterobacte
24	1027	99.5	286	2	06W9J21 enterobacte
25	1027	99.5	286	2	06W9J22 enterobacte
26	1027	99.5	286	2	06W9J23 enterobacte
27	1027	99.5	286	2	06W9J24 enterobacte
28	1027	99.5	286	2	06W9J25 enterobacte
29	1027	99.5	286	2	06W9J26 enterobacte
30	1027	99.5	286	2	06W9J27 enterobacte
31	1027	99.5	286	2	06W9J28 enterobacte

32	1027	99.5	286	2	06W9J1 enterobacte
33	1027	99.5	286	2	06W9J2 zymomonas m
34	1027	99.5	286	2	06W9J3 acinetobact
35	1027	99.5	286	2	06W9J4 citrobacter
36	1027	99.5	286	2	06W9J5 klebsiella
37	1027	99.5	286	2	06W9J6 shigella fl
38	1027	99.5	286	2	06W9J7 neisseria m
39	1027	99.5	286	2	06W9J8 salmonella
40	1027	99.5	286	2	06W9J9 serratia ma
41	1027	99.5	286	2	06W9J10 enterobacte
42	1027	99.5	286	2	06W9J11 enterobacte
43	1027	99.5	286	2	06W9J12 enterobacte
44	1027	99.5	286	2	06W9J13 enterobacte
45	1027	99.5	286	2	06W9J14 enterobacte

ALIGNMENTS

RESULT 1	ALIGNMENTS
ID 06W9J5; PRELIMINARY; PRT; 229 AA.	
AC 06W9J5; PRELIMINARY; PRT; 229 AA.	
DT 05-JUL-2004 (TREMBlrel. 27, Created)	
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)	
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)	
DE Beta-lactamase (Fragment).	
GN Name=blatm;	
OS Klebsiella oxytoca.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Klebsiella.	
OX NCBI_Taxid=571;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=MISC126;	
RA Ober C.A., Goldstone C.M., Gordon D.M., Riley M.A.;	
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AY265885; AAP93843.1; --	
DR HSP; P00807; IKGE.	
DR InterPro; IPR000871; Beta_lactamase_A.	
DR PRINTS; PR00118; BLACTAMASE.	
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.	
FT NON_TER 1 1	
FT NON_TER 229 229	
SQ SEQUENCE 229 AA; 23067 MW; C85582C2617F4467 CRC64;	
Query Match 100.0%; Score 1032; DB 2; Length 229;	
Best Local Similarity 100.0%; Pred. No. 1.3e-77;	
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 HPELVKVKDABDQAGARVGITIEDLNSGKTLSEFRPERPPMSTFVLLCGAVLSRID 60	
DB 2 HPELVKVKDABDQAGARVGITIEDLNSGKTLSEFRPERPPMSTFVLLCGAVLSRID 61	
QY 61 AGOBLGRIRHSQNDIVESPVTEKHLTDGATVRELCSAATMSDNTAAILLTIGGP 120	
DB 62 AGOBLGRIRHSQNDIVESPVTEKHLTDGATVRELCSAATMSDNTAAILLTIGGP 121	
QY 121 KELTAFILNMGDHYTRLDWPELNEALPNDERDTTVMVAATTLTKLLTGLTLTASRQ 180	
DB 122 KELTAFILNMGDHYTRLDWPELNEALPNDERDTTVMVAATTLTKLLTGLTLTASRQ 181	
QY 181 QIIMMEADKVAAGPLRSALPA 202	
DB 182 QIIMMEADKVAAGPLRSALPA 203	
RESULT 2	
ID 06W9J4; PRELIMINARY; PRT; 232 AA.	
AC 06W9J4; PRELIMINARY; PRT; 232 AA.	
DT 05-JUL-2004 (TREMBlrel. 27, Created)	
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)	

DT 05-JUN-2004 (TRENKLEL 27, Last annotation update)
DE Beta-lactamase (Fragment).
CN Name-blattm;
OS Haefnia alvei
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Haefnia.
OX NCBI_TaxID=569;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISC198;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY265886; AAP93844.1; --
DR HSSP: P00807; IKGE.
DR InterPro: IPR000871; Beta_lactamase_A.
DR PRINTS: PR00118; BLACTAMASEA
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 232
FT NON_TER 1 1
FT 232
FT 232 AA; 25380 MW; 305DFD885582C261 CRC64;
SQ SEQUENCE

Query Match	100.0%;	Score 1032;	DB 2;	Length 232;
Best Local Similarity	100.0%;	Pred. No. 1.3e-77;		
Matches 202; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	HEPTLVKVDADQELGARVGYIELDNSKLTIESRPERPPMNSTFVYLICGAVSRID	60
Db	2	HEPTLVKVDADQELGARVGYIELDNSKLTIESRPERPPMNSTFVYLICGAVSRID	61
Qy	61	AGQEQIGRRIRHSQNDLVEYSPVTEKHLLDGTQVTELCSAAITMSDNTAANILLTTIGCP	120
Db	62	AGQEQIGRRIRHSQNDLVEYSPVTEKHLLDGTQVTELCSAAITMSDNTAANILLTTIGCP	121
Qy	121	KELTAALAHNGDHVTLDRWEPELNEAIPNDRDPTTTPVAMATTIRKLLTGEILLTLASRQ	180
Db	122	KELTAALAHNGDHVTLDRWEPELNEAIPNDRDPTTTPVAMATTIRKLLTGEILLTLASRQ	181
Qy	181	QLIDMWEADKVAGPILRSALPA 202	
Db	182	QLIDMWEADKVAGPILRSALPA 203	

RESULT 3	
Q6MWT8	
ID Q6MWT8	PRELIMINARY; PRT; 241 AA.
AC Q6MWT8;	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE Beta-lactamase (Praguent).	
GN Name=blATEM;	
OS Klebsiella pneumoniae.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Klebsiella.	
NCBI_TaxID=573;	
XX	

RC STRAIN=MISC112;
RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBD databases.
DR EMBL: AY265882; AAP93440.1; -
DR HSSP: P00807; 1KGE
DR InterPro: IPR001466; Beta_lactamase.
DR InterPro: IPR000871; Beta_lactamase_A.
DR Pfam: PF00144; Beta_lactamase_1.
DR PRINTS: PR00118; BLACTAMSEA.
DR PROSITE: PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1 1
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26407 MW; 38DE2AFDF0C5E807D CRC64;

Query Match	100.0%;	Score 1032;	DB 2;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 1.4e-77;		

Matches	202:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
QY	1	HPETLVKKAEDQLGARVGIIEIDLSNGKILLESRRPRERPPMSTFVLLISGAVLSRID	60						
Db	7	HPETLVKKAEDQLGARVGIIEIDLSNGKILLESRRPRERPPMSTFVLLISGAVLSRID	66						
QY	61	AGQSGRRIHYSQNDLVEYSPYTEKHLTDGWTRELCSAITISDNRNAILLTIGSP	120						
Db	67	AGQSGRRIHYSQNDLVEYSPYTEKHLTDGWTRELCSAITISDNRNAILLTIGSP	126						
QY	121	KELTAFLHNMGDHYTRLDPRWEPELNEAIPNDRDITTMFVMAATTIRKLLTIGELLTLASRQ	180						
Db	127	KELTAFLHNMGDHYTRLDPRWEPELNEAIPNDRDITTMFVMAATTIRKLLTIGELLTLASRQ	186						
QY	181	QLIDIMKADKVAAGPLIRGALPA	202						
Db	187	QLIDIMKADKVAAGPLIRGALPA	208						

RESULT 4	
Q6WMY3	
ID Q6WMY3	PRELIMINARY; PRT; 242 AA

	DT	05-JUL-2004 (TEMBLrel_27, Created)
	DT	05-JUL-2004 (TEMBLrel_27, Last sequence update)
	DT	05-JUL-2004 (TEMBLrel_27, Last annotation update)
	DE	Beta-lactamase (Fragment).
	DE	Name=BlatEM;
	OS	Escherichia coli.
	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
	OC	Enterobacteriaceae; Escherichia.
	OX	NCB1_TaxID=562;
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=TA005;	
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;	
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL, AY655887; AAP93845.1; --	
DR	HSP; P08087; 1KGE	
DR	InterPro: IPR001456; Beta_lactamase.	
DR	InterPro: IPR000871; Beta_lactamase_A.	
DR	Pfam: PF00114; Beta_lactamase; 1.	
DR	PRINTS: PR00118; BLACTAMASE.	
DR	PROSITE: PS00146; BETA_LACTAMASE_A; 1.	
FT	NON_TER	1
ET	NON_TER	1
Q0	SEQUENCE	242 AA; 26554 MW; 38C3DFAB8A5A3807D CRC64;

Query Match	100.0%;	Score 1032;	DB 2;	Length 242;
Best Local Similarly	100.0%;	Pred. No. 1.4e-77;		
Matches 202; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	HEPILTKVXDABEQIGARVGYIELDNGSKILIESRPERPMMSTFVILICGAVSRID	60
Db	8	HPETLVKVDABEQIGARVGYIELDNGSKILIESRPERPMMSTFVILICGAVSRID	67
Qy	61	AGQEQGRRIHYSQNDLVEYSPVTEKHLLDGTWTVELCSAIIYMSDNTAANLLTTIGP	120
Db	68	AGQEQGRRIHYSQNDLVEYSPVTEKHLLDGTWTVELCSAIIYMSDNTAANLLTTIGP	127
Qy	121	KELTAFLAHMGDHTRLDRWEPELNEAIPNDERDPTTMEVAMATTLRKLLTGEELITLASRQ	180
Db	128	KELTAFLAHMGDHTRLDRWEPELNEAIPNDERDPTTMEVAMATTLRKLLTGEELITLASRQ	187
Qy	181	QLIDMWEADKVAGPLLRSALPA 202	
Db	188	QLIDMWEADKVAGPLLRSALPA 209	

RESULT 5	
Q6KB67	
ID Q6KB67	PRELIMINARY;
AC Q6KB67;	PRT; 285 AA


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DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
NCBI_TaxID=4513;
RX
RM
SEQUENCE FROM N.A.
RC TISSUE=first leaf;
RA Jansen C., Korell M., Beckey C., Biedenkopf D., Kogel K.H.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ717739; CAG30723.1; -.
DR HSSP; P08087; 1AQJ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hypothetical protein.
FT NON TER 285
SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQGVYIEIDLSGKILSFRRPFRPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKQADQDQGVYIEIDLSGKILSFRRPFRPMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLYEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANILLTTIGCP 120
DB 84 AGQQLGRRIHYSONDLYEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANILLTTIGCP 143
QY 121 KEITAFILNMGDHYTRLDRWPEPELNEALPNDERDTMPVANAATLTKLLTGELLTLASRQ 180
DB 144 KEITAFILNMGDHYTRLDRWPEPELNEALPNDERDTMPVANAATLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRSALPA 202
DB 204 QLIDWMEADKVAGPLRSALPA 225

RESULT 6
ID Q38058 PRELIMINARY; PRT; 286 AA.
AC Q38058;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta lactamase.
GN Name=bla;
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
NCBI_TaxID=10847;
RX
RM
SEQUENCE FROM N.A.
RC MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-X;
RA Henrich B., Schmidtberger B.;
RL "A variant of phiX174 gene E-based positive selection vectors with
enhanced lytic potential.";
RL Gene 154:51-54 (1995).
DR EMBL; Z35638; CAA84692.1; -.
DR PIR; S47061; S47061.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
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SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQGVYIEIDLSGKILSFRRPFRPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKQADQDQGVYIEIDLSGKILSFRRPFRPMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLYEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANILLTTIGCP 120
DB 84 AGQQLGRRIHYSONDLYEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANILLTTIGCP 143
QY 121 KEITAFILNMGDHYTRLDRWPEPELNEALPNDERDTMPVANAATLTKLLTGELLTLASRQ 180
DB 144 KEITAFILNMGDHYTRLDRWPEPELNEALPNDERDTMPVANAATLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRSALPA 202
DB 204 QLIDWMEADKVAGPLRSALPA 225

RESULT 7
ID 000626 PRELIMINARY; PRT; 286 AA.
AC 000626; 008022; 008102; 009393; 009396; 009397; 009398; 009399;
AC 009400; 009401; 009402; 009403; 009404; 009405; 009406; 009407;
AC 009408; 009481; 009482; 009483; 009490; 057339;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Beta-lactamase.
OS Staphylococcus aureus.
OG Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RX
RM
SEQUENCE FROM N.A.
RC PLSMID=J3356/POX7/3, and J3356/POX7/1;
RX MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plae.1995.0005;
RA Needham C., Noble W.C., Dyke K.G.;
RL "The staphylococcal insertion sequence IS25 is active.";
RL Plasmid 34:198-205 (1995).
DR EMBL; U36912; AAB39957.1; -.
DR EMBL; U36911; AAB39956.1; -.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASE.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADQDQGVYIEIDLSGKILSFRRPFRPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKQADQDQGVYIEIDLSGKILSFRRPFRPMSTFVLLCGAVLSRID 83
QY 61 AGQQLGRRIHYSONDLYEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANILLTTIGCP 120
DB 84 AGQQLGRRIHYSONDLYEYSPVTEKHLTDGMTVRELCSAIIWSDNTAANILLTTIGCP 143
QY 121 KEITAFILNMGDHYTRLDRWPEPELNEALPNDERDTMPVANAATLTKLLTGELLTLASRQ 180
DB 144 KEITAFILNMGDHYTRLDRWPEPELNEALPNDERDTMPVANAATLTKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLRSALPA 202
DB 204 QLIDWMEADKVAGPLRSALPA 225
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RESULT 8

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079CL6 PRELIMINARY; PRT; 286 AA.
ID 079CL6
AC 079CL6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-lactamase.
GN Name-bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylotiales;
OC Methylotiales; Methylobacillus.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Seebrijski I.G., Vassin V.M., Tsygankov Y.D.;
RT "Two new members of the BioB superfamily: cloning, sequencing and
RT expression of bioB genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum."
RL Gene 175:15-22 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Seebrijski I., Vassin V., Tsygankov Y.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U31280; AAC4581.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKKVDAEDQGVGVYIEIDLSGKILSFREPERPMMSTFKVLGAVLSRID 60
DB 24 HPELVKKVDAEDQGVGVYIEIDLSGKILSFREPERPMMSTFKVLGAVLSRID 83
QY 61 AGGOLGRIRHYSONDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTGGP 120
DB 84 AGGOLGRIRHYSONDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTGGP 143
QY 121 KeltafLHMGDHTRLDRWEPELNEAIPNDRDPTMPVAVATTIRKLLTGELLTLASRQ 180
DB 144 KeltafLHMGDHTRLDRWEPELNEAIPNDRDPTMPVAVATTIRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAGPLRSALPA 202
DB 204 QLIIMWEADKVAGPLRSALPA 225

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RESULT 9

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079DR3 PRELIMINARY; PRT; 286 AA.
ID 079DR3
AC 079DR3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name-bla; Synonyms=blatEM-116;
OS Escherichia coli.
OC Plasmid pBP4, and Plasmid pCAPs.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pBP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breitling F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=pCAPs;
RX MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the csp gene
RT Escherichia coli."
RL Anal. Biochem. 257:203-209 (1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey."
RL J. Clin. Microbiol. 42:2902-2906 (2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; Y12694; CAA73226.1; -.
DR EMBL; AJ001614; CAA04868.1; -.
DR EMBL; AY425988; AAQ95605.1; -.
DR HSSP; P00807; IALQ.
DR GO; GO:000800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolyase; plasmid; signal.
FT SIGNAL 23
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

```

```

Query Match 100.0%; Score 1032; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1,7e-77;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HPELVKKVDAEDQGVGVYIEIDLSGKILSFREPERPMMSTFKVLGAVLSRID 60
DB 24 HPELVKKVDAEDQGVGVYIEIDLSGKILSFREPERPMMSTFKVLGAVLSRID 83
QY 61 AGGOLGRIRHYSONDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTGGP 120
DB 84 AGGOLGRIRHYSONDLYEVSPTVEKHLTDGMTVRELCSAITSNDTAAVLLTTGGP 143
QY 121 KeltafLHMGDHTRLDRWEPELNEAIPNDRDPTMPVAVATTIRKLLTGELLTLASRQ 180
DB 144 KeltafLHMGDHTRLDRWEPELNEAIPNDRDPTMPVAVATTIRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAGPLRSALPA 202
DB 204 QLIIMWEADKVAGPLRSALPA 225

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RESULT 10

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038212 PRELIMINARY; PRT; 225 AA.
ID 038212
AC 038212;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Bacteriophage f1-R208 amplicillinase gene mutation. (fragment).

```

OS Bacteriophage f1.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
NC NCB1_TaxID=10863;
RN [1]
RP SEQUENCE FROM N.A.
RK MEDLINE=86278026; PubMed=3525535;
RA Topal M.D., Badie J.S., Conrad M.;
RT "O-6-methylguanine mutation and repair is nonuniform: Selection for
DNA most interactive with O-6-methylguanine.";
RL J. Biol. Chem. 261:9879-9885 (1986).
DR EMBL, M14017; AAA32208.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASRA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 225 AA; 25022 MW; 009BF841D618BA09 CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 225;
Best Local Similarity 99.0%; Pred. No. 3.3e-77;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 24 HPELVKVKADBDQAGVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANILLTTIGSP 120
DB 84 AGQEQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANILLTTIGSP 143
QY 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDPTMVAATTIRKLLTGELITLASRQ 180
DB 144 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDPTMVAATTIRKLLTGELITLASRQ 203
QY 181 QLIDMMEADKVAAGPLRSALPA 202
DB 204 QLIDMMEADKVAAGPLRSALPA 225

RESULT 11
Q6PRU7 PRELIMINARY; PRT; 232 AA.
AC Q6PRU7;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Inhibitor-resistant TEM beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Bacterichia.
NC NCB1_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U3;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY553761; AAS86427.1; -.
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASRA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
SQ SEQUENCE 232 AA; 25558 MW; 5791CD285EB70BB0 CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 232;
Best Local Similarity 99.0%; Pred. No. 3.4e-77;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 15 HPELVKVKADBDQAGVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 74
QY 61 AGQEQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANILLTTIGSP 120
DB 75 AGQEQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANILLTTIGSP 134
QY 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDPTMVAATTIRKLLTGELITLASRQ 180
DB 135 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDPTMVAATTIRKLLTGELITLASRQ 194
QY 181 QLIDMMEADKVAAGPLRSALPA 202
DB 195 QLIDMMEADKVAAGPLRSALPA 216

RESULT 12
Q84H50 PRELIMINARY; PRT; 255 AA.
AC Q84H50;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Bacterichia.
NC NCB1_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Box A.T.A., Pauw A., Leverstein-vanhal M.A.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY130282; AAN05026.1; -.
DR HSSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASRA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 255;
Best Local Similarity 99.0%; Pred. No. 3.8e-77;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADBDQAGVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 60
DB 12 HPELVKVKADBDQAGVGYIELDLSGKILSFPRPERPMMSTFKVLLCGAVLSRID 71
QY 61 AGQEQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANILLTTIGSP 120
DB 72 AGQEQLGRRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATWSDNTAANILLTTIGSP 131
QY 121 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDPTMVAATTIRKLLTGELITLASRQ 180
DB 132 KELTAFILNMGDHYTRLDRMEPELNEAIPNDRDPTMVAATTIRKLLTGELITLASRQ 191
QY 181 QLIDMMEADKVAAGPLRSALPA 202
DB 192 QLIDMMEADKVAAGPLRSALPA 213

RESULT 13
Q84H49 PRELIMINARY; PRT; 261 AA.
AC Q84H49;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).

OS Klebsiella oxytoca.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 ON NCBI_TaxID=571;
 RP SEQUENCE FROM N.A.
 RA Box A.T.A., Paauw A., Leverstein-vanhalp M.A., Verhoef J., Fluit A.C.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY130283; AA05027.1; -.
 DR HSSP; O9R435; 1HTZ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1 1
 FT SEQUENCE 261 AA; 28738 MW; 4F748F773A08CBB CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 261;
 Best Local Similarity 99.0%; Pred. No. 3.9e-77;
 Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDVGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRD 60
 DB 12 HPELVKVKADQDVGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRD 71
 QY 61 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
 DB 72 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 131
 QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 132 KETLAFLLHMGDHYTRLDRWEPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 191
 QY 181 QLIDMEADKVAAGPLRSALPA 202
 DB 192 QLIDMEADKVAAGPLRSALPA 213

RESULT 14
 Q6PRU6 PRELIMINARY; PRT; 264 AA.
 AC Q6PRU6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DS TEM Beta-lactamase (Fragment).
 OS Acinetobacter sp. U11.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 ON NCBI_TaxID=269266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=U11;
 RC Ghandali S., Hosseini-Mazinan S.M.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY583762; AAS6428.1; -.
 DR HSSP; P00807; 1ALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1 1
 FT SEQUENCE 264 AA; 28986 MW; A4F071CF7489352C CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 264;
 Best Local Similarity 99.0%; Pred. No. 4e-77;
 Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDVGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRD 60

DB 12 HPELVKVKADQDVGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRD 71
 QY 61 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
 DB 72 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 131
 QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 132 KETLAFLLHMGDHYTRLDRWEPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 191
 QY 181 QLIDMEADKVAAGPLRSALPA 202
 DB 192 QLIDMEADKVAAGPLRSALPA 213

RESULT 15
 Q6QIV0 PRELIMINARY; PRT; 281 AA.
 ID Q6QIV0;
 AC Q6QIV0;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DS TEM-1 beta-lactamase (Fragment).
 GN Name=BlatEM-1;
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 ON NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
 RA Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY538700; AAS46846.1; -.
 DR EMBL; AY538701; AAS46847.1; -.
 DR EMBL; AY538702; AAS46848.1; -.
 DR EMBL; AY538698; AAS46844.1; -.
 DR HSSP; P00807; 1ALQ.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 281 281
 FT SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;

Query Match 99.5%; Score 1027; DB 2; Length 281;
 Best Local Similarity 99.0%; Pred. No. 4.3e-77;
 Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADQDVGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRD 60
 DB 24 HPELVKVKADQDVGARVGYIELDLSGKILSFREPERPPMSTFKVLLCGAVLSRD 83
 QY 61 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 120
 DB 84 AGOQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP 143
 QY 121 KETLAFLLHMGDHYTRLDRWEPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 180
 DB 144 KETLAFLLHMGDHYTRLDRWEPELNEAI PNDERDTMPVAMATTLRKLLTGELLTLASRQ 203
 QY 181 QLIDMEADKVAAGPLRSALPA 202
 DB 204 QLIDMEADKVAAGPLRSALPA 225

Search completed: June 10, 2005, 10:57:03
 Job time : 68.6736 secs

Qy 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228

RESULT 3
 ADJ67709
 ID ADJ67709 standard; protein; 263 AA.
 AC ADJ67709;
 XX
 XX 20-MAY-2004 (first entry)
 DE Escherichia coli TEM-1 beta-lactamase.
 XX
 XX fragment complementation system; marker protein;
 KM multiple genetic element incorporation; antibiotic resistance;
 KM beta-lactam derivative activation; anti-tumour compound;
 KM functional reassembly; protein-protein interaction; proteome interaction;
 KM immunoglobulin variable region; immune cell protein; CD40;
 KM phosphorylation-regulated cell signal transducer; TEM-1 beta-lactamase;
 KM enzyme.
 XX
 XX Escherichia coli.
 OS
 XX
 XX US2004038317-A1.
 PV
 XX 26-FEB-2004.
 PD
 XX 22-SEP-2003; 2003US-00668778.
 PF
 XX 15-MAR-1999; 99US-0124339P.
 PR 25-MAY-1999; 99US-0135926P.
 PR 13-JAN-2000; 2000US-0175968P.
 PR 15-MAR-2000; 2000US-00526106.
 XX
 XX (KALO-) KALOBIO INC.
 PA
 PI Balint RF, Her J;
 DR WPI; 2004-203222/19.
 DR N-PSDB; ADJ67708.
 XX
 XX
 PT Fragment complementation system for detecting immunoglobulin epitope, has
 PT first oligopeptide containing N-terminal fragment with C-terminal break-
 PT point, second oligopeptide containing C-terminal fragment with N-terminal
 PT break-point.
 XX
 PS Disclosure; SEQ ID NO 2; 47bp; English.

CC efficiently detects multiple interaction between extracellular and
 CC intracellular protein with high throughput format. This is the amino acid
 CC sequence of antibiotic resistance enzyme TEM-1 beta-lactamase that can be
 CC used as a selectable gene in the fragment complementation system of the
 CC invention.
 XX
 XX SQ Sequence 263 AA;
 XX
 XX Query Match 100.0%; Score 1170; DB 8; Length 263;
 XX Best Local Similarity 100.0%; Pred. No. 8.5e-117;
 XX Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HBETLVKVKDADQAGAVGYIELDNLNSGKILSFRPERPFWMTFKVLLCGAVLSRID 60
 DB 1 HBETLVKVKDADQAGAVGYIELDNLNSGKILSFRPERPFWMTFKVLLCGAVLSRID 60
 Qy 61 AGQEBOLGRIRIHSQNDLYEYSPVTEKHLTDGTTVELCSAATMGSNDTANLLTTIGP 120
 DB 61 AGQEBOLGRIRIHSQNDLYEYSPVTEKHLTDGTTVELCSAATMGSNDTANLLTTIGP 120
 Qy 121 KETLAFILNMGGDVTRLDRWEPENLEAI PNDRDITTPVAMATTLRKLLTGELTLASRQ 180
 DB 121 KETLAFILNMGGDVTRLDRWEPENLEAI PNDRDITTPVAMATTLRKLLTGELTLASRQ 180

Qy 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 181 QUIDMMEADKVAGPILRSALPAGWFIADKSGAGERSGIIAALGPDG 228

RESULT 4
 AAW16634
 ID AAW16634 standard; protein; 264 AA.
 AC AAW16634;
 XX
 XX 09-AUG-1997 (first entry)
 DT
 XX
 XX Beta-lactamase (including signal peptide).
 DE
 XX
 XX Gene directed enzyme prodnrg therapy; GDEPT;
 KM virus directed enzyme prodnrg therapy; VDEPT; beta-lactamase; cancer;
 KM HIV; inflammation.
 KW
 XX
 XX Escherichia coli.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label= Sig_peptide

PN MO9719180-A2.
 XX
 XX 29-MAY-1997.
 PD
 XX
 XX 19-NOV-1996; 96WO-GB002845.
 PF
 XX
 XX 20-NOV-1995; 95GB-00023703.
 PR
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PA
 PI Dev I, Moore JT, Ohmstede C;
 XX
 XX WPI; 1997-298117/27.
 DR N-PSDB; AAT66736.
 DR
 XX
 XX Molecular chimera for gene or virus directed enzyme prodnrg therapy -
 PT useful for treatment of cancer, viral infection or inflammation.
 PT
 XX
 XX Example; Page 28; 38bp; English.
 PS
 XX Escherichia coli beta-lactamase (AAW16634), including the signal peptide,
 CC is the expression product of a molecular chimera, designated pCMV-BL
 CC (AAT66737), in which the beta-lactamase gene is under control of the CMV
 CC intermediate/early promoter. Vectors consisting of a transcriptional

CC regulatory DNA sequence linked to a beta-lactamase gene can be used for
 CC enzyme producing therapy. Expression of the beta-lactamase in a targeted
 CC cell allows conversion of a producing into an agent toxic to the cell for
 CC treatment of cancer. viral (e.g. HIV) infection or inflammation.
 CC Secretion of the enzyme has the advantage of increasing neighbouring cell
 CC kill

XX Sequence 264 AA;

Query Match 100.0%; Score 1170; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 8.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILIESFRPERPMMSTFKVLLCGAVLSRID 60

Db 2 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILIESFRPERPMMSTFKVLLCGAVLSRID 61

QY 61 AGOGLGRRIHYSQNDLVESPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 120

Db 62 AGOGLGRRIHYSQNDLVESPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 121

QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELTLASRQ 180

Db 122 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELTLASRQ 181

QY 181 QLIDMMEADKVAGPULRSALPAGWFIADKSGAGERSGRTIATLGPDG 228

Db 182 QLIDMMEADKVAGPULRSALPAGWFIADKSGAGERSGRTIATLGPDG 229

RESULT 5

AAW18680
 ID AAW18680 standard; protein; 264 AA.

XX AAW18680;

DT 13-AUG-1997 (first entry)

XX Intracellularly-expressed beta-lactamase.

XX Producing therapy; gene directed enzyme producing therapy; GDEPT;

KM virus directed enzyme producing therapy; VDEPT; lung cancer;

KW beta-lactamase; PCMV-delIBL.

XX Escherichia coli.

OS

XX W09719183-A2.

PN

XX 29-MAY-1997.

PD

XX 19-NOV-1996; 96WO-GB002846.

PF

XX 20-NOV-1995; 95GB-00023703.

PR

XX (GLAX) GLAXO GROUP LTD.

PA

XX Dev I, Moore JT, Sethna PB;

PI

XX WPI; 1997-298118/27.

XX N-PSDB; AAT70311.

PT DNA construct for gene-directed enzyme producing therapy of lung cancer -

XX comprises lung- or neuroendocrine-specific promoter controlling

XX expression of producing-converting enzyme.

XX Example 811; Page 32-34; 53pp; English.

XX The intracellular form (AAW18680) of TEM beta-lactamase is expressed by

XX PCMV-delIBL (AAT70311) in which a PCR-amplified beta-lactamase coding

XX sequence, minus the signal sequence, is placed under control of the

XX intermediate/early promoter of cytomegalovirus. Intracellular beta-

XX lactamase constructs, placed under control of promoter/enhancer elements

XX of lung-associated protein or neuroendocrine marker protein genes, can be

CC used in novel chimaeric molecules for use in producing therapy of lung

CC cancer

XX Sequence 264 AA;

Query Match 100.0%; Score 1170; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 8.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILIESFRPERPMMSTFKVLLCGAVLSRID 60

Db 2 HPEITLVKVKADBDQAGARVGYIEIDLNSGKILIESFRPERPMMSTFKVLLCGAVLSRID 61

QY 61 AGOGLGRRIHYSQNDLVESPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 120

Db 62 AGOGLGRRIHYSQNDLVESPVTEKHLTDGATVRELCSAAITMSDNTAANLLTTIGCP 121

QY 121 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELTLASRQ 180

Db 122 KELTAFILNMGDHVTRLDRWEPELNEALPNDERDTTVPVAMATTLRKLLTGELTLASRQ 181

QY 181 QLIDMMEADKVAGPULRSALPAGWFIADKSGAGERSGRTIATLGPDG 228

Db 182 QLIDMMEADKVAGPULRSALPAGWFIADKSGAGERSGRTIATLGPDG 229

RESULT 6

AAW1575
 ID AAW1575 standard; protein; 286 AA.

XX AAW1575;

DT 10-MAR-2003 (revised)

DT 04-JUN-1993 (first entry)

XX Ampicillin resistance protein.

XX CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;

KM xenobiotics; circular; chimeric cytochrome P450IA1.

XX Homo sapiens.

OS

XX US5180666-A.

PN

XX 19-JAN-1993.

PD

XX 27-JUN-1991; 91US-00721775.

PF

XX 27-JUN-1991; 91US-00721775.

PR

XX (UYWA-) UNIV WAYNE STATE.

PA

XX States JC, Hines RM, Novak RF;

PI

XX WPI; 1993-052845/06.

XX N-PSDB; AAQ36498.

XX In vitro method for testing mutagenicity of a chemical - by metabolising

XX chemical cell line consisting of transformed fibroblasts having

XX detectable cytochrome P450 mixed function oxidase activity and detecting

XX gene damage.

PT Disclosure; Col 21-24; 24pp; English.

XX The expression constructs PRNH127 and PRNH155 contain identical sequences

XX but were constructed using different strategies (see AAQ36498). The

XX constructs comprise exons 2-7 of human CYP1A1 gene under the control of

XX the inducible mouse metallothionein (MMT-1) promoter. The constructs also

XX contain an open reading frame in the opposite orientation to the

XX cytochrome P450 exons. This ORF encodes ampicillin resistance. The

XX constructs are suitable for transformation of human fibroblasts derived

XX from the xeroderma pigmentosum group A. Cultures of the transformed

XX fibroblasts can be used to test substances for mutagenicity. The presence

CC of the inducible cytochrome P450 gene allows metabolism of the substance
 CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
 CC field.)

XX Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGRVGYIELDLSGKILSFRRPFRPMSFTFYLLCGAVLSRID 60
 DB 24 HPEITLVKVKDADQAGRVGYIELDLSGKILSFRRPFRPMSFTFYLLCGAVLSRID 83
 QY 61 AGQELGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQELGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
 QY 181 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDG 228
 DB 204 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDG 251

RESULT 7

AAR97619 ID AAR97619 standard; protein; 286 AA.

XX AAR97619;

DT 20-AUG-1996 (first entry)

XX Secretory beta-lactamase.

DE Gene therapy; gene directed enzyme prodnug therapy; GDEPT;

KM virus directed enzyme prodnug therapy; VDEPT; prodnug activation;

KW cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;

KV beta-lactamase; cephalosporin.

XX Synthetic.

OS WO9616179-A1.

XX 30-MAY-1996.

XX 20-NOV-1995; 95WO-GB002716.

XX 18-NOV-1994; 94GB-00023367.

XX (WELL) WELLCOME FOUND LTD.

XX Dev IK, Moore JT, Ohmsted C;

XX WPI; 1996-268615/27.

XX N-PSDB; AAT29220.

XX Molecular chimaera for use in enzyme gene therapy - is activated in a

XX target cell to express a secreted enzyme which cleaves a prodnug in a

XX outside the cell into a cytotoxic or cytostatic agent.

XX Example 3; Page 57-58; 73pp; English.

XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct
 CC PCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under
 CC the control of the intermediate/early cytomegalovirus promoter. Beta-
 CC lactamase delivery to mammalian cells confers sensitivity to
 CC cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations
 CC resulted in s.c. tumour regression in mice bearing A549 tumours. Survival
 CC of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours
 CC was increased upon i.t. injection of the secretory beta-lactamase DNA

CC construct
 XX Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 9.5e-117;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDADQAGRVGYIELDLSGKILSFRRPFRPMSFTFYLLCGAVLSRID 60
 DB 24 HPEITLVKVKDADQAGRVGYIELDLSGKILSFRRPFRPMSFTFYLLCGAVLSRID 83
 QY 61 AGQELGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 120
 DB 84 AGQELGRIRIHVSQNDLVEYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTIGSP 143
 QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 180
 DB 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDRDITMPVAMATTIRKLLTGELTLASRQ 203
 QY 181 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDG 228
 DB 204 QLIDWMEADKVAGPLLRSGALPAGWFIADKSGAGERSGRIITAAIGPDG 251

RESULT 8

AAR96423 ID AAR96423 standard; protein; 286 AA.

XX AAR96423;

DT 25-MAR-2003 (revised)

DT 25-NOV-1996 (first entry)

XX Cytochrome P450 (CYP1A1 construct).

KW cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;

KV metabolism.

XX Homo sapiens.

XX US5525482-A.

XX 11-JUN-1996.

XX 15-NOV-1994; 94US-00339658.

XX 27-JUN-1991; 91US-00721775.

XX 09-DEC-1992; 92US-00990295.

XX (UYWA-) UNIV WAYNE STATE.

XX Hines RN, Novak RF, States JC;

XX WPI; 1996-286397/29.

XX N-PSDB; AAT30354.

XX Testing chemicals for cytotoxicity to human by detecting gene damage -

XX using recombinant fibroblasts transformed with cytochrome P450 gene under

XX control of inducible promoter.

XX Disclosure; Col 17-24; 26pp; English.

XX The present sequence is encoded by a chimeric mouse metallothionein-
 CC cytochrome P450IA1 (CYP1A1) expression construct. Two clones, pRNM127 and
 CC pRNM15, were isolated by different methods and which both had the same
 CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity
 CC of humans to a chemical. The method comprises exposing human fibroblast
 CC cells normally not including any cytochrome P450 activity to potentially
 CC toxic chemicals. The cells having been transformed to express cytochrome
 CC P450, under the control of a controllable promoter through the CYP1A1
 CC gene, upon exposure to the chemical in vitro. The chemical is metabolised
 CC intracellularly into a cytochrome metabolite by oxidation within the

fibroblasts through the intracellular cytochrome P450 mixed function oxidase enzymes expressed by the cells. Gene damage in the test cells is detected as an indication of cytotoxicity of the chemical. (Updated on 25 -MAR-2003 to correct PF field.)

Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXKDADQIGARVGYIEIDNSGKILIESFRPERPPMSTFKVLLCGAVLSRID 60

DB 24 HPEITLVKXKDADQIGARVGYIEIDNSGKILIESFRPERPPMSTFKVLLCGAVLSRID 83

QY 61 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 120

DB 84 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 143

QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBLLTLASRQ 180

DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBLLTLASRQ 203

QY 181 QLIDMMEADKVAGPLLRGALPAGWFIADKSGAGRGSRGIIAALGPDG 228

DB 204 QLIDMMEADKVAGPLLRGALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 9

AAW16635
ID AAW16635 standard; protein; 286 AA.

AAW16635;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (no signal peptide).

XX Gene directed enzyme prodng therapy; GDEPT;

KW virus directed enzyme prodng therapy; VDEPT; beta-lactamase; cancer;

KM HIV; inflammation.

OS Escherichia coli.

XX WO9719180-A2.

XX PD 29-MAY-1997.

XX PF 19-NOV-1996; 96WO-GB002845.

XX PR 20-NOV-1995; 95GB-00023703.

XX PA (GLAXO) GLAXO GROUP LTD.

XX FI Dev I, Moore JT, Ohmstede C;

XX WIPI; 1997-298117/27.

XX DR N-PSDB; AAT66737.

XX PT Molecular chimera for gene or virus directed enzyme prodng therapy -

XX useful for treatment of cancer, viral infection or inflammation.

XX Example; Page 26; 38pp; English.

XX Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,

is the expression product of a molecular chimera, designated pCMV-delBL

(AAT66738), in which the beta-lactamase gene is under control of the CMV

intermediate/early promoter. Vectors consisting of a transcriptional

regulatory DNA sequence linked to a beta-lactamase gene can be used for

enzyme prodng therapy. Intracellular expression of the beta-lactamase in

a targeted cell allows conversion of a prodng into an agent toxic to

the cell for treatment of cancer, viral (e.g. HIV) infection or

inflammation

XX Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKXKDADQIGARVGYIEIDNSGKILIESFRPERPPMSTFKVLLCGAVLSRID 60

DB 24 HPEITLVKXKDADQIGARVGYIEIDNSGKILIESFRPERPPMSTFKVLLCGAVLSRID 83

QY 61 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 120

DB 84 AGOEOLGRIRHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAAILLTTIGSP 143

QY 121 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBLLTLASRQ 180

DB 144 KELTAFILNMGDHYTRLDRWEPELNEAIPNDRDTTTPVAAVATTLRKLLTGBLLTLASRQ 203

QY 181 QLIDMMEADKVAGPLLRGALPAGWFIADKSGAGRGSRGIIAALGPDG 228

DB 204 QLIDMMEADKVAGPLLRGALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 10

AAW18679
ID AAW18679 standard; protein; 286 AA.

AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodng therapy; gene directed enzyme prodng therapy; GDEPT;

KW virus directed enzyme prodng therapy; VDEPT; lung cancer;

KM beta-lactamase; pCMV-BL.

XX OS Escherichia coli.

XX PN WO9719183-A2.

XX PD 29-MAY-1997.

XX PF 19-NOV-1996; 96WO-GB002846.

XX PR 20-NOV-1995; 95GB-00023703.

XX PA (GLAXO) GLAXO GROUP LTD.

XX FI Dev I, Moore JT, Sethna PB;

XX WIPI; 1997-298118/27.

XX DR N-PSDB; AAT70309.

XX PT DNA construct for gene-directed enzyme prodng therapy of lung cancer -

XX comprises lung- or neuroendocrine-specific promoter controlling

XX expression of prodng-converting enzyme.

XX Example 8ii; Page 26-27; 53pp; English.

XX The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-

BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is

placed under control of the intermediate/early promoter of

cytomegalovirus. Secretory beta-lactamase constructs, placed under

control of promoter/enhancer elements of lung- associated protein or

neuroendocrine marker protein genes, can be used in novel chimeric

CC molecules for use in prodrg therapy of lung cancer
XX
SQ Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYIELDNSGKILESPPRPERPMMSTFKYLGGAVLSRID 60
DB 24 HPELVKVDADQAGVGYIELDNSGKILESPPRPERPMMSTFKYLGGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFLEHMGDHYTRLDRWEPLENEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLEHMGDHYTRLDRWEPLENEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 203
QY 161 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIIAALGPDG 228
DB 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIIAALGPDG 251

RESULT 11

AAV08529
ID AAV08529 standard; protein; 286 AA.

AC AAV08529;
XX
DT 03-AUG-1999 (first entry)

DE Vector pASK75 beta-1a protein.

XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;
KW tetracycline repressor; tetracycline promoter; luminescence; luxCDABE;
KW insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;
KW allergy.

OS Synthetic.

PN WO925866-A1.

XX 27-MAY-1999.

PF 11-NOV-1998; 98WO-FI000873.

PR 14-NOV-1997; 97FI-00004235.

PA (KORP/) KORPELA M.

PA (KARP/) KARP M.

PA (KURIT/) KURITTU J.

PI Korpela M, Karp M, Kurittu J;

DR MPI, 1999-338015/28.

DR N-PSDB; AAV72418.

PT Assaying for tetracycline using recombinant prokaryotic cells.

PS Disclosure; Page 47-48; 67pp; English.

CC This invention describes a novel tetracycline assay that uses recombinant
CC prokaryotic cells comprising a luciferase gene under the transcriptional
CC control of a tetracycline repressor and tetracycline promoter and
CC involves the detection of luminescence emitted from the cells. The assay
CC can be used to distinguish tetracycline form other microbial agents. The
CC invention also describes a novel plasmid comprising either the luxCDABE
CC genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA)
CC from Tn10, or the insect luciferase gene, a tetracycline repressor (TetR)
CC and a tetracycline promoter (TetA) from Tn10. The tetracycline assay
CC method can be used for the determination of tetracycline in a sample,

CC e.g. to study the dosage and penetration of the medicine. The method can
CC also be used to test cheese production, as cheese making bacteria are not
CC able to work in the presence of tetracycline. The method can also be used
CC to determine the presence or concentration of antibiotics in foodstuffs,
CC e.g. for allergic people. The present assay method does not rely on the
CC growth of microbes as do conventional tests, and so is much more rapid.
CC The present assay is also more sensitive, as even a small amount of
CC luminescence can be detected

XX Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVDADQAGVGYIELDNSGKILESPPRPERPMMSTFKYLGGAVLSRID 60
DB 24 HPELVKVDADQAGVGYIELDNSGKILESPPRPERPMMSTFKYLGGAVLSRID 83
QY 61 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 120
DB 84 AGOEOLGRRIHYSQNDLVEYSPVTEKHLTDGWTVELCSAATMSDNTANLLTTIGSP 143
QY 121 KELTAFLEHMGDHYTRLDRWEPLENEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 180
DB 144 KELTAFLEHMGDHYTRLDRWEPLENEALPNDERDTTMAPVAMATTIRKLLTGELTLASRQ 203
QY 161 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIIAALGPDG 228
DB 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIIAALGPDG 251

RESULT 12

AAV10442
ID AAV10442 standard; protein; 286 AA.

AC AAV10442;

XX 01-DEC-2000 (first entry)

DE Expression vector pSEX1562 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

PN DE19900635-A1.

XX 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA Breitling F, Pouscka A, Moldenhauer G;

DR MPI, 2000-499832/45.

DR N-PSDB; AAV71430.

PT Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 3; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (I); and (ii) binding the antibody to antigens (Ag). The

invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I K(K) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the bla protein contained in the expression vector pSEX11G2 which contains the bla protein, Neo-R and protein G described in the method of the invention

Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVAADQAGVGYIELDLSGKILSPRPFRPMPSTFKVLLCGAVLSRID 60
DB 24 HPELVKVAADQAGVGYIELDLSGKILSPRPFRPMPSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVERELCSAITWSDNTAANLLTTTGGP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVERELCSAITWSDNTAANLLTTTGGP 143
QY 121 KELTAFILNMGDHVTLRDMPPELNEALPNDERDTMPVAAATTKRLITGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTLRDMPPELNEALPNDERDTMPVAAATTKRLITGELLTLASRQ 203
QY 181 QUIDMWEADKVAGPLLRSAALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QUIDMWEADKVAGPLLRSAALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 13

AAB10438

ID AAB10438 standard; protein; 286 AA.

AAB10438;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11L4 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71428.

XX Selecting monoclonal antibodies, by expressing them on the surface of
PT hybridomas attached to antibody-binding protein, then reaction with
XX antibody library.

Claim 16; Fig 1; 22pp; German.

This invention describes a novel method for the selection of monoclonal antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding protein (I); and (ii) binding the antibody to antigens (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I K(K) molecule; an antibody-binding site of proteins A, G, L or Ig, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select Mab with specificity for particular antigens. Mab can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in Mab selection. This sequence represents the Neo-R protein contained in the expression vector pSEX11L4 which contains the bla protein, Neo-R and protein G described in the method of the invention

Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 3; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.5e-117;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVAADQAGVGYIELDLSGKILSPRPFRPMPSTFKVLLCGAVLSRID 60
DB 24 HPELVKVAADQAGVGYIELDLSGKILSPRPFRPMPSTFKVLLCGAVLSRID 83
QY 61 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVERELCSAITWSDNTAANLLTTTGGP 120
DB 84 AGQELGRRIHYSQNDLVEYSPVTEKHLTDGWTVERELCSAITWSDNTAANLLTTTGGP 143
QY 121 KELTAFILNMGDHVTLRDMPPELNEALPNDERDTMPVAAATTKRLITGELLTLASRQ 180
DB 144 KELTAFILNMGDHVTLRDMPPELNEALPNDERDTMPVAAATTKRLITGELLTLASRQ 203
QY 181 QUIDMWEADKVAGPLLRSAALPAGWFIADKSGAGERSGRTIAALGPDG 228
DB 204 QUIDMWEADKVAGPLLRSAALPAGWFIADKSGAGERSGRTIAALGPDG 251

RESULT 14

AAB10440

ID AAB10440 standard; protein; 286 AA.

AAB10440;

DT 01-DEC-2000 (first entry)

DE Expression vector pSEX11G2 bla protein.

XX Expression vector; antibody binding protein; monoclonal antibody; Neo-R;

KM B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.

OS Synthetic.

DE19900635-A1.

PD 13-JUL-2000.

PF 11-JAN-1999; 99DE-01000635.

PR 11-JAN-1999; 99DE-01000635.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Breitling F, Poustka A, Moldenhauer G;

DR WPI: 2000-499832/45.

DR N-PSDB; AAA71429.

XX Selecting monoclonal antibodies, by expressing them on the surface of

PT hybridomas attached to antibody-binding protein, then reaction with
PT antibody library.

PS Claim 16; Fig 2; 22pp; German.

CC This invention describes a novel method for the selection of monoclonal
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma
CC cells to produce antibody-producing hybridomas such that the antibodies
CC are presented at the surface of the hybridomas by an antibody-binding
CC protein (i); and (ii) binding the antibody to antigens (Ag). The
CC invention also describes antibody-binding proteins (i) that comprise a
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)
CC molecule; an antibody-binding site of proteins A, G, L or Ig; and the
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)
CC or CD52. The method is used to select Mab with specificity for particular
CC antigens. Mab can be selected without separate culture of hybridomas, and
CC selection can be made against many antigens in a library, optionally on
CC the basis of strength of affinity for a particular antigen. Complex
CC mixtures of hybridomas can be used for selection, reducing the time and
CC cost involved in Mab selection. This sequence represents the bla protein
CC protein contained in the expression vector pSEX102 which contains the
CC bla protein, Neo-R and protein G described in the method of the invention
CC
SQ Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 3; Length 286;

Best Local Similarity 100.0%; Pred. No. 9.5e-117; Mismatches 0; Indels 0; Gaps 0;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLCGAVLSRID 83
QY 61 AGQEQGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTTIGP 120
DB 84 AGQEQGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAAATTLRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB 204 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

RESULT 15

AAB50898 ID AAB50898 standard; protein; 286 AA.

XX AAB50898;

XX 20-MAR-2001 (first entry)

DE Protein encoded by bla resistance marker of integration vector pLO12306.

XX bla resistance marker; recombinant host cell; saccharification;
KW fermentation; polysaccharase; oligosaccharide degradation; celz gene;
KW glucanase; integration vector; pLO12306.

XX Unidentified.

OS WO200071729-A2.

XX 30-NOV-2000.

XX 26-MAY-2000; 2000WO-US014773.

XX 26-MAY-1999; 99US-0136376P.

XX (UVFL) UNIV FLORIDA RES FOUND.

PI Ingram LO, Zhou S;
XX
DR MPI: 2001-032043/04.
DR N-PSDB; AAC91455.

XX Recombinant host cells useful for producing polysaccharase for degrading
PT oligosaccharides, comprises a first heterologous polynucleotide encoding
PT polysaccharase under control of surrogate promoter.

PS Disclosure: Page 82-83; 87pp; English.

CC The present sequence is given in a specification relating to a
CC recombinant host cell suitable for simultaneous saccharification and
CC fermentation. The host cell contains at least one heterologous
CC polynucleotide encoding a polysaccharase under the transcriptional
CC control of a surrogate promoter capable of increasing expression of the
CC polysaccharase. The host cell also contains a second heterologous
CC polynucleotide encoding a secretory polypeptide to facilitate the
CC secretion of the expressed polysaccharase. The recombinant host cell is
CC useful for producing polysaccharase which is useful for enzymatically
CC degrading oligosaccharides such as lignocellulose, hemicellulose,
CC cellulose, pectin or their combinations, and fermenting the product to
CC ethanol, by simultaneous saccharification and fermentation processes. The
CC present sequence is encoded by an integration vector which was introduced
CC into cells to generate recombinant host cells. The vector contains a
CC surrogate promoter from *Zymomonas mobilis*, the celz gene from *Erwinia*
CC chrysanthemi, resistance markers bla and tet, and *Klebsiella oxytoca*
CC target sequence

SQ Sequence 286 AA;

Query Match 100.0%; Score 1170; DB 4; Length 286;

Best Local Similarity 100.0%; Pred. No. 9.5e-117; Mismatches 0; Indels 0; Gaps 0;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKQADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLCGAVLSRID 60
DB 24 HPEITLVKQADBDQAGVGYIELDINSKILSFPRPERPMMSTFKVLCGAVLSRID 83
QY 61 AGQEQGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTTIGP 120
DB 84 AGQEQGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDNTAAILTTTIGP 143
QY 121 KETLAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAAATTLRKLLTSELTLASRQ 180
DB 144 KETLAFILNMGDHVTRLDRWEPELNEAIPNDERDTMPVAAATTLRKLLTSELTLASRQ 203
QY 181 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 228
DB 204 QLIDMMEADKVAAGPLRSALPAGWFIADKSGAGRGSRGIIAALGPDG 251

Search completed: June 10, 2005, 10:49:14

Job time : 89.4014 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2005, 10:35:06 ; Search time 16.6267 Seconds
(without alignment)

1319,408 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_228

Perfect score: 1170
Sequence: 1 HPETLVKVKDAEDQLGARVQ.....KSGAGERGSRGIIALGPDDG 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	286	2	TS1301
2	1170	100.0	286	2	beta-lactamase (EC
3	1170	100.0	286	4	S47061
4	1165	99.6	286	1	beta-lactamase (EC
5	1165	99.6	286	4	PNECP
6	1152	98.5	286	2	beta-lactamase (EC
7	1151	98.4	286	2	S30113
8	1145	97.9	286	2	S60310
9	1143	97.7	286	2	S60311
10	1139	97.4	286	2	J01546
11	828	70.8	265	2	S00464
12	826	70.6	286	2	S16146
13	826	70.6	286	2	A60679
14	822	70.3	265	2	S02434
15	822	70.3	286	1	A44998
16	819	70.0	286	2	A37200
17	818	69.9	286	2	A60632
18	815	69.7	265	2	A60448
19	813	69.5	279	2	A24469
20	803.5	68.7	287	1	A44966
21	768	65.6	286	1	A44958
22	610	53.1	298	2	A41381
23	484.5	41.4	302	2	S35188
24	483.5	41.3	291	2	S42075
25	483	41.3	281	2	D95395
26	480.5	41.1	293	2	S04649
27	479.5	41.0	263	2	A54543
28	477.5	40.8	306	2	G69674
29	476.5	40.7	306	2	S47330

30	475.5	40.6	294	2	S16553	beta-lactamase (EC
31	474.5	40.6	288	2	J01136	beta-lactamase (EC
32	470.5	40.2	304	2	A49789	beta-lactamase (EC
33	470.5	40.2	304	2	A35001	beta-lactamase (EC
34	467.5	40.0	306	1	B45822	beta-lactamase (EC
35	467.5	40.0	314	2	S06967	beta-lactamase (EC
36	463.5	39.6	288	2	J50755	beta-lactamase (EC
37	462	39.5	305	2	A61156	beta-lactamase (EC
38	462	39.5	305	2	A57002	beta-lactamase (EC
39	462	39.5	305	2	A60680	beta-lactamase (EC
40	456.5	39.0	311	2	U00520	beta-lactamase (EC
41	455	38.9	276	2	DH0268	beta-lactamase (EC
42	452.5	38.7	291	2	JP0074	beta-lactamase (EC
43	449.5	38.4	263	2	S23929	beta-lactamase (EC
44	448.5	38.3	294	2	S19006	beta-lactamase (EC
45	445.5	38.1	307	1	PMBSL	beta-lactamase (EC

ALIGNMENTS

```

RESULT 1
TS1301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C/Accession: TS1301
R/WACH, A.; BRACHAT, A.; ALBERTSSEUL, C.; REBISCHUNG, C.; PHILIPSEN, P.
A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharon
A/Reference number: Z09587
A/Accession: TS1301
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-286 <WAC>
A/Cross-references: EMBL:AJ002683; PDB:CAA05686.1
C/Genetics:
A/Gene: bla
C/Superfamily: beta-lactamase I
C/Keywords: hydrolase

Query Match          100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 8e-94;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HPETLVKVKDAEDQLGARVGIIEIDLNSGKILSFRRPFRPPMSTFRVLLCGAVLSRID 60
        |||||
DB      24 HPETLVKVKDAEDQLGARVGIIEIDLNSGKILSFRRPFRPPMSTFRVLLCGAVLSRID 83

QY      61 AGQEQIGRRIRHSQNDLYEVSPTVEKHLTDGWTVEICSAATITMSDNTAANLTLTIGSP 120
        |||||
DB      84 AGQEQIGRRIRHSQNDLYEVSPTVEKHLTDGWTVEICSAATITMSDNTAANLTLTIGSP 143

QY      121 KELTAFILNMGDHVTLRDWEPELNEAIPNDRDITMVAATTKLITGELTLTASRQ 180
        |||||
DB      144 KELTAFILNMGDHVTLRDWEPELNEAIPNDRDITMVAATTKLITGELTLTASRQ 203

QY      161 QIIDMEADKVAAGPILRSALPGWFIADKSGAGERGSRGIIALGPDDG 228
        |||||
DB      204 QIIDMEADKVAAGPILRSALPGWFIADKSGAGERGSRGIIALGPDDG 251

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C/Species: phage phi-X174
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S47061
R/Henrich, B.; Schmidtberger, B.
A/Submitted to the EMBL Data Library, July 1994
A/Description: A variant of phix174 gene B-based positive selection vectors with enhanced
A/Reference number: S47060
A/Accession: S47061

```


RESULT 5
140905
beta-lactamase (EC 3.5.2.6) - synthetic
C:Species: synthetic
A:Note: Cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. cynod
C:Date: 15-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Oct-2000
C:Accession: I40905
R:Taylor, J.; Stearman, R.S.; Urcatani, B.B.
Plasmid 29, 241-244, 1993
A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.
A:Reference number: 140904; MUID:93361581; PMID:7689234
A:Accession: I40905
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <RES>
A:Cross-references: EMBL:U21228; NID:g885956; PIDD:AAA70411.1; PID:g885958
C:Keywords: hydrolase

Query Match 99.6%; Score 1165; DB 4; Length 286;
Best Local Similarity 99.1%; Pred. No. 2.2e-93;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

Qy 61 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFIHMGGHVTRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELITLASRQ 180
Db 144 KELTAFIHMGGHVTRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELITLASRQ 203

Qy 181 QUIDMMEADKVAAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QUIDMMEADKVAAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 6
560312
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60312
R:Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60312
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <KHA>
A:Cross-references: EMBL:X65254; NID:g296955; PIDD:CAA46346.1; PID:g296956
C:Superfamily: beta-lactamase I

Query Match 98.5%; Score 1152; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 2.9e-92;
Matches 223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

Qy 61 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFIHMGGHVTRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELITLASRQ 180
Db 144 KELTAFIHMGGHVTRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELITLASRQ 203

Qy 181 QUIDMMEADKVAAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228

Db 204 QUIDMMEADKVAAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 7
530113
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFE04
C:Species: *Klebsiella pneumoniae*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S30113
R:Abillat, C.; Lourenco-Vital, J.; Goussard, S.; Courvalin, P.
Mol. Gen. Genet. 235, 113-121, 1992
A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple-
A:Reference number: S30112; MUID:93062798; PMID:1331747
A:Accession: S30113
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <MAB>
A:Cross-references: UNIPROT:P00810; EMBL:X64523; NID:g43797; PIDD:CAA45828.1; PID:g43798
C:Genetics:
A:Gene: bla(TEM-3)
A:Genome: plasmid
C:Superfamily: beta-lactamase I
C:Keywords: antibiotic resistance; hydrolase

Query Match 98.4%; Score 1151; DB 2; Length 286;
Best Local Similarity 97.8%; Pred. No. 3.5e-92;
Matches 223; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

Qy 61 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120
Db 84 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 143

Qy 121 KELTAFIHMGGHVTRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELITLASRQ 180
Db 144 KELTAFIHMGGHVTRLDRWBEPLNEAIPNDRDITMPVAMATTIRKLITGELITLASRQ 203

Qy 181 QUIDMMEADKVAAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
Db 204 QUIDMMEADKVAAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 8
560310
extended spectrum beta-lactamase CAZ-2 - *Klebsiella pneumoniae*
C:Species: *Klebsiella pneumoniae*
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C:Accession: S60310
R:Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A:Reference number: S60310; MUID:93037315; PMID:1416873
A:Accession: S60310
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <KHA>
A:Cross-references: EMBL:X65252; NID:g296951; PIDD:CAA46344.1; PID:g296952
C:Superfamily: beta-lactamase I

Query Match 97.9%; Score 1145; DB 2; Length 286;
Best Local Similarity 97.4%; Pred. No. 1.2e-91;
Matches 222; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 60
Db 24 HPELVKVDADQAGARVGYIELDNSGKILSFRRPFRPMSTFKVLLCGAVLSRID 83

Qy 61 AGQOLGRRIHYSQNDLYEYSPVTEKHLTDGWTVELCSAATMSDNTAANLLTTIGSP 120

Db 84 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPDG 228
Db 204 QLIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPDG 251

RESULT 9

S60311
beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60311; F37392; F00498
R:Chanal, C.; Poupart, M.C.; Siroc, D.; Labia, R.; Siroc, J.; Cluzel, R.
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60311
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CAA>
A/Cross-references: UNIPROT:Q99224; EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g2969
R:Toimasky, M.E.
A/Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans
A/Reference number: A37392; MUID:91172904; PMID:1963948
A/Accession: F37392
A/Molecule type: DNA
A/Residues: 1-32 <TOL>
A/Cross-references: CB:M5547; NID:g155010; PIDN:AAA9408.1; PID:g155016
C/Genetics:
A/Gene: TEM-bla
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
Query Match 97.7%; Score 1143; DB 2; Length 286;
Best Local Similarity 96.9%; Pred. No. 1.7e-91;
Matches 221; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 120
Db 84 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPDG 228
Db 204 QLIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPDG 251

RESULT 10

QJ01546
Bla protein - Salmonella typhimurium plasmid NTP16
N/Alternate names: beta lactamase homolog
C/Species: Salmonella typhimurium
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: QJ01546
R:Canon, P.M.; Strike, P.
A/Title: Complete nucleotide sequence and gene organization of plasmid NTP16.
A/Reference number: QJ01548; MUID:92383313; PMID:13325061
A/Accession: QJ01546
A/Status: translation not shown

A/Molecule type: DNA
A/Residues: 1-286 <CAN>
A/Cross-references: UNIPROT:Q8L2F9
C/Genetics:
A/Genome: plasmid
C/Superfamily: beta-lactamase I
Query Match 97.4%; Score 1139; DB 2; Length 286;
Best Local Similarity 97.4%; Pred. No. 3.9e-91;
Matches 222; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 60
Db 24 HPEITLVKVDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 83
QY 61 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 120
Db 84 AGOQOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 143
QY 121 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 180
Db 144 KETLAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPDG 228
Db 204 QLIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPDG 251

RESULT 11

S00464
beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453
N/Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
C/Species: Escherichia coli
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993
C/Accession: S00464
R:Barthelmy, M.; Peduzzi, J.; Labia, R.
Biochem. J. 251, 73-79, 1988
A/Title: Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-lactamase (SHV-
A/Reference number: S00464; MUID:88268817; PMID:3260490
A/Accession: S00464
A/Molecule type: protein
A/Residues: 1-265 <BAR>
C/Genetics:
A/Genome: plasmid
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
Query Match 70.8%; Score 828; DB 2; Length 265;
Best Local Similarity 69.0%; Pred. No. 3.1e-64;
Matches 156; Conservative 33; Mismatches 37; Indels 0; Gaps 0;

QY 2 PETLVKVDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
Db 2 PETLVKVDADQAGARVGYIELDLSNGKILSFRRPFRPMMSTFKVLLCGAVLSRID 61
QY 62 GOEOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 121
Db 62 GOEOLGRRHHYSONDLVYSPVTEKHLTDGWTVELCSAAITMSDNTAANLLTTTGGP 121
QY 122 ELTAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 181
Db 122 ELTAFLLHMGDHYTRLDRWPEPELNEAIPNDERDPTTVPVAAATTLRKLLTGSELLTTLASRQ 181
QY 182 LIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPD 227
Db 182 LIDWMEADKVAAGPLLRSLALPAGWFIADKSGAGERSGGIITAAIGPD 227

RESULT 12

S16146
beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella pneumoniae plasmids
N/Alternate names: beta-lactamase SHV2A
C/Species: Klebsiella pneumoniae

C/Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Oct-1999
C/Accession: S16146; A35395; S18767
R/Protein: A.; Scheinling, J.; Melzer, B.; Warmatz, K.; Leusch, H.G.
J. Gen. Microbiol. 137, 569-578, 1991
A/Title: Molecular characterization of a new plasmid-encoded SHV-type beta-lactamase (SHV-2) from *Enterobacter cloacae* strain 137
A/Reference number: S16146; MUID:91237320; PMID:2033379
A/Accession: S16146
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <PO>
A/Cross-references: EMBL:X53917, NID:g43795; PIDN:CAA37813.1; PID:g43796
A/Experimental source: plasmid pZMP1
R/Lee, K.Y.; Hopkins, J.D.; Syman, M.
J. Bacteriol. 172, 3229-3236, 1990
A/Title: Direct involvement of IS26 in an antibiotic resistance operon.
A/Reference number: A35395; MUID:90264317; PMID:2160941
A/Accession: A35395
A/Molecule type: DNA
A/Residues: 1-30, '1', '32-286 <LEB>
A/Cross-references: GB:X62115; NID:g48908; PIDN:CAA44025.1; PID:g48990
A/Experimental source: plasmid BMH77
C/GeneticB:
A/Gene: blaS2A
A/Genome: plasmid
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 70.6%; Score 826; DB 2; Length 286;
Best Local Similarity 68.6%; Pred. No. 5.1e-64;
Matches 155; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

QY 2 PETLVKVDADQDQARVGYIELDLSGKILSPRPERPFPMSSTFKVLLCGAVLSRIDA 61
DB 23 PQLPQIKQSQSLSGRGMTLMDLSSGRTLTAMRADERFPMSSTFKVLLCGAVLARVDA 82
QY 62 GQEQLRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGPK 121
DB 83 GDEQLERKIHRRQDLDVYSPVSEKHLADGMTVGLCAAIITMSDNSANLLLATVGGPA 142
QY 122 ELTAFIHNMGDHVTRLDMWEPFLNEAIPNDEBDTTPVPMATTLTKLTLGELLTASRQ 181
DB 143 GLTAFIRQIGDVTRLDMWETELNEALPGDARDITTPASMAATLTKLTLTSQRLSARQ 202
QY 182 LIDWMEADKVAGPLRLSALPAGMFIADKSGAGERSGRIIALGPD 227
DB 203 LIDWMEADKVAGPLRLSALPAGMFIADKSGAGERSGRIIALGPD 248

RESULT 13
A/Accession: A60679
A/Species: *Salmonella typhimurium*
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Aug-2004
C/Accession: A60679
R/Garbarz-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.C.
Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A/Title: Nucleotide sequence of SHV-2 beta-lactamase gene.
A/Reference number: A60679; MUID:90351141; PMID:2201259
A/Accession: A60679
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-286 <GAR>
A/Cross-references: GB:L47119; NID:g972890; PIDN:AAA75015.1; PID:g972891
C/GeneticB:
A/Genome: plasmid
C/Superfamily: Beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase
R/1-21/Domain: signal sequence #status predicted <SIG>

Query Match 70.6%; Score 826; DB 2; Length 286;
Best Local Similarity 68.6%; Pred. No. 5.1e-64;
Matches 155; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

QY 2 PETLVKVDADQDQARVGYIELDLSGKILSPRPERPFPMSSTFKVLLCGAVLSRIDA 61
DB 23 PQLPQIKQSQSLSGRGMTLMDLSSGRTLTAMRADERFPMSSTFKVLLCGAVLARVDA 82
QY 62 GQEQLRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGPK 121
DB 83 GDEQLERKIHRRQDLDVYSPVSEKHLADGMTVGLCAAIITMSDNSANLLLATVGGPA 142
QY 122 ELTAFIHNMGDHVTRLDMWEPFLNEAIPNDEBDTTPVPMATTLTKLTLGELLTASRQ 181
DB 143 GLTAFIRQIGDVTRLDMWETELNEALPGDARDITTPASMAATLTKLTLTSQRLSARQ 202
QY 182 LIDWMEADKVAGPLRLSALPAGMFIADKSGAGERSGRIIALGPD 227
DB 203 LIDWMEADKVAGPLRLSALPAGMFIADKSGAGERSGRIIALGPD 248

RESULT 14
S02434
beta-lactamase (EC 3.5.2.6) SHV-2 - *Escherichia coli*
C/Species: *Escherichia coli*
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C/Accession: S02434
R/Bartelme, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R.
FBS Lett. 231, 217-220, 1988
A/Title: Single amino acid substitution between SHV-1 beta-lactamase and cefotaxime-hydr
A/Reference number: S02434; MUID:88196385; PMID:3129309
A/Accession: S02434
A/Molecule type: protein
A/Residues: 1-265 <BAR>
C/Superfamily: beta-lactamase I
C/Keywords: antibiotic resistance; hydrolase

Query Match 70.3%; Score 822; DB 2; Length 265;
Best Local Similarity 68.6%; Pred. No. 1e-63;
Matches 155; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

QY 2 PETLVKVDADQDQARVGYIELDLSGKILSPRPERPFPMSSTFKVLLCGAVLSRIDA 61
DB 2 PQLPQIKQSQSLSGRGMTLMDLSSGRTLTAMRADERFPMSSTFKVLLCGAVLARVDA 61
QY 62 GQEQLRRIHYSQNDLVESPVTEKHLTDGMTVRELCSAATMSDNTANLLTTIGPK 121
DB 83 GDEQLERKIHRRQDLDVYSPVSEKHLADGMTVGLCAAIITMSDNSANLLLATVGGPA 121
QY 122 ELTAFIHNMGDHVTRLDMWEPFLNEAIPNDEBDTTPVPMATTLTKLTLGELLTASRQ 181
DB 143 GLTAFIRQIGDVTRLDMWETELNEALPGDARDITTPASMAATLTKLTLTSQRLSARQ 202
QY 182 LIDWMEADKVAGPLRLSALPAGMFIADKSGAGERSGRIIALGPD 227
DB 203 LIDWMEADKVAGPLRLSALPAGMFIADKSGAGERSGRIIALGPD 248

RESULT 15
A44998
beta-lactamase (EC 3.5.2.6) SHV-2 - *Klebsiella pneumoniae* pBP60
C/Species: *Klebsiella pneumoniae*
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C/Accession: A44998; S12703
R/Huletsky, A.; Couture, F.; Levesque, R.C.
Antimicrob. Agents Chemother. 34, 1725-1732, 1990
A/Title: Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.
A/Reference number: A44998; MUID:91136192; PMID:2285285
A/Accession: A44998
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <HUI>
A/Cross-references: UNIPROT:P14558; GB:M95179; NID:9150488; PIDN:AAA2526.1; PID:g150489
R/Protein: A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
A/Title: Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase (bla(SHV-2))
A/Reference number: S12703; MUID:90370479; PMID:2395654

A/Accession: S12703
A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-286 <POD>

A/Cross-references: EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790

C/Genetics:

A/Genome: plasmid

C/Superfamily: Beta-lactamase I

C/Keywords: antibiotic resistance; hydrolase

Query Match 70.3%; Score 822; DB 1; Length 286;

Best Local Similarity 68.6%; Pred. No. 1,1e-63;

Matches 155; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

```
QY      2 PETLVKVDADQDQAGRVGYIELDLSGKILESFRPERPMMSTFKYLLCGAVLSRIDA 61
      | : : : | | | | : : : | : : : | | | | : : : | | | | : : : |
Db     23 PQLLEQITLSQSQLSGRVGMTEMDLASGRTLTAWRADERFPMSTFKYVLCGAVLARVDA 82
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
QY      62 GQEQIGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTANLLLTGTGPK 121
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
Db     83 GDEQLERKIHRYQDLDVYSPVSEKHLADGMTVGELCAAATMSDNSANLLLTATVGGPA 142
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
QY     122 ELTAFIHHMGDHVTRLDWPEPELNEAIPNDERDPTMPYMATLRKLLTGELTLASRQ 181
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
Db     143 GLTAPLRQIGDNVTRLDWETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQR 202
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
QY     182 LIDWMEADKVGAPLRSALPAGWFIADKSGAGERSGRIIALGPD 227
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
Db     203 LIGMMVDNRVAGPLIRSVLPAGWFIADKSGASRGARGIVALLGPN 248
      | : : : | | | | : : : | | | | : : : | | | | : : : | | | |
```

Search completed: June 10, 2005, 10:58:49

Job time : 17.6267 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2005, 10:23:36 ; Search time 76.3841 Seconds
(without alignments)
1528.512 Million cell updates/sec

Title: US-10-668-778-2_COPY_1_228

Perfect score: 1170
Sequence: 1 HPELTVKVKADMDQAGARVG.....KSGAGERSRGIIALGPDG 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_crembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	229	2	Q6WMY5 Klebsiella
2	1170	100.0	232	2	Q6WMY4 Hafnia alve
3	1170	100.0	241	2	Q6WMY8 Klebsiella
4	1170	100.0	242	2	Q6WMY3 Escherichia
5	1170	100.0	285	2	Q6KB67 hordeum vul
6	1170	100.0	286	2	Q38058 bacterioph
7	1170	100.0	286	2	Q00626 staphylococ
8	1170	100.0	286	2	Q79CL6 methylobact
9	1170	100.0	286	2	Q79DR3 Escherichia
10	1165	99.6	255	2	Q84H50 Escherichia
11	1165	99.6	261	2	Q84H49 Klebsiella
12	1165	99.6	264	2	Q6PRU6 acinetobact
13	1165	99.6	281	2	Q6OIV0 serratia ma
14	1165	99.6	282	2	Q6OIV1 serratia ma
15	1165	99.6	286	1	BLAT_ECOLI
16	1165	99.6	286	1	BLAT_SALTI
17	1165	99.6	286	1	BLAT_SALTI
18	1165	99.6	286	2	Q8V43 Klebsiella
19	1165	99.6	286	2	Q8V43 Klebsiella
20	1165	99.6	286	2	Q93A77 Escherichia
21	1165	99.6	286	2	Q6A253 haemophilus
22	1165	99.6	286	2	Q6LBN9 pseudomonas
23	1165	99.6	286	2	Q6LCV6 neisseria g
24	1165	99.6	286	2	Q6TMH1 streptococc
25	1165	99.6	286	2	Q6UVM7 acinetobact
26	1165	99.6	286	2	Q6WJ74 Escherichia
27	1165	99.6	286	2	Q6WJ71 enterobacte
28	1165	99.6	286	2	Q6WJ72 zymomonas m
29	1165	99.6	286	2	Q6WJ73 acinetobact
30	1165	99.6	286	2	Q7B3X5 citrobacter
31	1165	99.6	286	2	Q7B899 klebsiella

32	1165	99.6	286	2	Q7BP57 shigella fl
33	1165	99.6	286	2	Q7BR75 neisseria m
34	1165	99.6	286	2	Q7DFY3 salmonella
35	1165	99.6	286	2	Q7DHD3 serratia ma
36	1165	99.6	286	2	Q799Y1 plasmid ppy
37	1165	99.6	286	2	Q7BVP8 Klebsiella
38	1162	99.3	234	2	Q6WMY6 citrobacter
39	1162	99.3	286	2	P78144 Escherichia
40	1162	99.3	286	2	Q8KSD2 Escherichia
41	1161	99.2	274	2	Q6Q4T6 pseudomonas
42	1161	99.2	277	2	Q9KHC0 Escherichia
43	1161	99.2	286	2	Q32372 capnocytoph
44	1161	99.2	286	2	Q8RPY9 enterobacte
45	1161	99.2	286	2	Q932Y6 pseudomonas

ALIGNMENTS

RESULT 1

ID	Q6WMY5	PRELIMINARY	PRT	229 AA
AC	Q6WMY5			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Beta-lactamase (Fragment).			
GN	Name=BLATEM;			
OS	Klebsiella oxyloca.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Klebsiella.			
OX	NCBI_TaxID=571;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MISC126;			
RA	Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;			
RL	Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY265885; AAP3843.1; -			
DR	HSP; P00807; IKGE.			
DR	Interpro; IPR000871; Beta_lactamase_A.			
DR	PRINTS; PR00118; BLACTAMASEA.			
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE	229 AA; 25067 MW; C85582C2617F4467 CRC64;		
Query Match				
Best local similarity 100.0%; Score 1170; DB 2; Length 229;				
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 HPELTVKVKADMDQAGARVGYIELDLNSGKTIESTFRPEERPFPMSTFKYLLCGAVLSRID			60
DB	2 HPELTVKVKADMDQAGARVGYIELDLNSGKTIESTFRPEERPFPMSTFKYLLCGAVLSRID			61
QY	61 AGOQLGRIRHVSQNDLVAYSPTKEKHTLDGWTVEILCSAATITMSDNTAANLLTTIGSP			120
DB	62 AGOQLGRIRHVSQNDLVAYSPTKEKHTLDGWTVEILCSAATITMSDNTAANLLTTIGSP			121
QY	121 KELTAFILNMGDHYRLDRMEPELNEAIPNDRDITMPVANAATTIRKLLTGELTLTASRQ			180
DB	122 KELTAFILNMGDHYRLDRMEPELNEAIPNDRDITMPVANAATTIRKLLTGELTLTASRQ			181
QY	181 QLIIDMEADKVAQPLIRSAALPAGWFIADKSGAGERSRGIIALGPDG 228			
DB	182 QLIIDMEADKVAQPLIRSAALPAGWFIADKSGAGERSRGIIALGPDG 229			
RESULT 2				
ID	Q6WMY4	PRELIMINARY	PRT	232 AA
AC	Q6WMY4			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			

DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Hafnia alvei.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Hafnia.
 CX NCBI_TaxID=563;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC139;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DB EMBL; AY265886; AAP93844.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 232
 SQ SEQUENCE 232 AA; 25380 MW; 3D5DFD85582C261 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 8.8e-87;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELTVKVAEDQAGAVGYIELDINSKILSFRRPERPPMSTFVLLCGAVLSRID 60
 DB 2 HPELTVKVAEDQAGAVGYIELDINSKILSFRRPERPPMSTFVLLCGAVLSRID 61
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAULLTTIGSP 120
 DB 62 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAULLTTIGSP 121
 QY 121 KELTAFLLNMGDHVTRLDRWPEPELNEAIPNDRDTPMPVAAATTLRKLLTGELLTLASRQ 180
 DB 122 KELTAFLLNMGDHVTRLDRWPEPELNEAIPNDRDTPMPVAAATTLRKLLTGELLTLASRQ 181
 QY 181 QLIWMEDAKVAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDG 228
 DB 182 QLIWMEDAKVAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDG 229

RESULT 3

ID Q6WMY8 PRELIMINARY; PRT; 241 AA.
 AC Q6WMY8;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Klebsiella pneumoniae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Klebsiella.
 CX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISC112;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DB EMBL; AY265882; AAP93840.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA; 26407 MW; 38DF2AFDF0C5807D CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 9.2e-87;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELTVKVAEDQAGAVGYIELDINSKILSFRRPERPPMSTFVLLCGAVLSRID 60
 DB 7 HPELTVKVAEDQAGAVGYIELDINSKILSFRRPERPPMSTFVLLCGAVLSRID 66
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAULLTTIGSP 120
 DB 67 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAULLTTIGSP 126
 QY 121 KELTAFLLNMGDHVTRLDRWPEPELNEAIPNDRDTPMPVAAATTLRKLLTGELLTLASRQ 180
 DB 127 KELTAFLLNMGDHVTRLDRWPEPELNEAIPNDRDTPMPVAAATTLRKLLTGELLTLASRQ 186
 QY 181 QLIWMEDAKVAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDG 228
 DB 187 QLIWMEDAKVAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDG 234

RESULT 4

ID Q6WMY3 PRELIMINARY; PRT; 242 AA.
 AC Q6WMY3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DB EMBL; AY265887; AAP93845.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR000871; Beta_lactamase.
 DR InterPro; IPR001466; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 242
 SQ SEQUENCE 242 AA; 26554 MW; 38C3DFA8A5A3807D CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 9.3e-87;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELTVKVAEDQAGAVGYIELDINSKILSFRRPERPPMSTFVLLCGAVLSRID 60
 DB 8 HPELTVKVAEDQAGAVGYIELDINSKILSFRRPERPPMSTFVLLCGAVLSRID 67
 QY 61 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAULLTTIGSP 120
 DB 68 AGOGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAITSNDTNAULLTTIGSP 127
 QY 121 KELTAFLLNMGDHVTRLDRWPEPELNEAIPNDRDTPMPVAAATTLRKLLTGELLTLASRQ 180
 DB 128 KELTAFLLNMGDHVTRLDRWPEPELNEAIPNDRDTPMPVAAATTLRKLLTGELLTLASRQ 187
 QY 181 QLIWMEDAKVAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDG 228
 DB 188 QLIWMEDAKVAGPLRLSALPAGWFIADKSGAGRGSGRTIAALGPDG 235

RESULT 5

ID Q6KB67 PRELIMINARY; PRT; 285 AA.
 AC Q6KB67;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 DE Beta-lactamase (Fragment).
 GN Name=blatEM;
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TA005;
 RA Obert C.A., Goldstone C.M., Gordon D.M., Riley M.A.;
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DB EMBL; AY265887; AAP93845.1; --
 DR HSSP; P00807; IKGE.
 DR InterPro; IPR000871; Beta_lactamase.
 DR InterPro; IPR001466; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 FT NON_TER 1
 FT NON_TER 285
 SQ SEQUENCE 285 AA; 30800 MW; 38C3DFA8A5A3807D CRC64;

DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothesis protein (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 NCBI_TaxID=4513;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=First leaf.
 RA Jansen C., Korell M., Ecker C., Biedenkopf D., Kogel K.H.;
 RL Submitted (May-2004) to the EMBL/Genbank/DDJ databases.
 DR EMBL; J071773; CAG30723.1; -.
 DR HSP; P0807; IAU.
 DR InterPro; IPR00146; Beta_lactamase.
 DR InterPro; IPR00871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Hypothetical protein.
 FT NON TER 285
 SQ SEQUENCE 285 AA; 31371 MW; A2F22753375FA930 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPMSSTFKVLLCGAVLSRID 60
 DB HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPMSSTFKVLLCGAVLSRID 83
 QY 61 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
 DB AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
 DB 84 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 180
 DB KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 203
 DB 181 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 204 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 6

Q38058 PRELIMINARY; PRT; 286 AA.
 ID Q38058
 AC Q38058;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta lactamase.
 GN Name=bla;
 OS Bacteriophage phi-X174.
 CC Viruses; ssDNA viruses; Microviridae; Microvirinae.
 NCBI_TaxID=10847;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95172401; PubMed=7867948; DOI=10.1016/0378-1119(94)00839-K;
 RA Henrich B., Schmidtberger B.;
 RT "A variant of phX174 gene B-based positive selection vectors with
 enhanced lytic potential."
 RL Gene 154:51-54(1995).
 DB EMBL; Z35638; CAA84692.1; -.
 DR PIR; S47061; S47061.
 DR HSP; Q9R435; IHTZ.
 DR InterPro; IPR00146; Beta_lactamase.
 DR InterPro; IPR00871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.

SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPMSSTFKVLLCGAVLSRID 60
 DB HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPMSSTFKVLLCGAVLSRID 83
 QY 61 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
 DB AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
 DB 84 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 180
 DB KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 203
 DB 181 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 204 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 7

ID Q00626 PRELIMINARY; PRT; 286 AA.
 AC Q00626; O08022; O08102; O09393; O09396; O09397; O09398; O09399;
 AC O09400; O09401; O09402; O09403; O09404; O09405; O09406; O09407;
 AC O09408; O09481; O09482; O09483; O09490; Q57339;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Beta-lactamase.
 OS Staphylococcus aureus.
 CC Plasmid J3356/POX7/3, and Plasmid J3356/POX7/1.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID=J3356/POX7/3, and J3356/POX7/1;
 RA MEDLINE=96422755; PubMed=8825372; DOI=10.1006/plas.1995.0005;
 RX Needham C., Noble W.C., Dyke K.G.;
 RT "The staphylococcal insertion sequence IS257 is active."
 RL Plasmid 34:198-205(1995).
 DR EMBL; U36912; AAB39957.1; -.
 DR EMBL; U36911; AAB39956.1; -.
 DR InterPro; IPR00146; Beta_lactamase.
 DR InterPro; IPR00871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASE.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KM Plasmid.
 KW Plasmid.
 SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPMSSTFKVLLCGAVLSRID 60
 DB HPELVKVKADADQAGVGYIELDLSGKILSFPRPERPMSSTFKVLLCGAVLSRID 83
 QY 61 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 120
 DB AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
 DB 84 AGQELGRIRIHSQNDLVEYSPVTEKHLTDGTVRELCSAATMSDNTAANLLTTIGCP 143
 QY 121 KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 180
 DB KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 203
 QY 144 KELTAFILNMGDHTVRLRWPEBELNEAIPNDRDITMPVMAATTIRKLLTGELTLASRQ 203
 DB 181 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDG 228
 DB 204 QLIIDMEADKVAAGPLRLSALPAGWFIADKSGAGERSGIIAALGPDG 251

RESULT 8

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079CL6 PRELIMINARY; PRT; 286 AA.
ID 079CL6
AC 079CL6
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-lactamase.
GN Name=bla;
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Methylotiales;
OC Methylotiales; Methylobacillus.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074643; PubMed=8917070; DOI=10.1016/0378-1119(96)00114-X;
RA Seebrijski I.G., Vassin V.M., Tsygankov Y.D.;
RT "Two new members of the B108 superfamily: cloning, sequencing and
RT expression of b108 genes of Methylobacillus flagellatum and
RT Corynebacterium glutamicum."
RL Gene 175:15-22(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Seebrijski I., Vassin V., Tsygankov Y.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U31280; AAC4581.1; -.
DR HSSP; P00807; IALO.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.le-86;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGEOGLGRRIHYSONDLYEVSPTVEKHLTDGMTVRELCSAIIITSDNTAAILTTIGCP 120
DB 84 AGEOGLGRRIHYSONDLYEVSPTVEKHLTDGMTVRELCSAIIITSDNTAAILTTIGCP 143
QY 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGERSGIIAALGPDG 251

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RESULT 9

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079DR3 PRELIMINARY; PRT; 286 AA.
ID 079DR3
AC 079DR3
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Mutant extended-spectrum beta-lactamase precursor (EC 3.5.2.6).
GN Name=bla; Synonyms=blatm-116;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=K-12;
RA Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;
RL Submitted (AUG-1991) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; PLASMID=pprP4;
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,
RA Little M., Breitling F.;
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=PCAP8;
RX MEDLINE=96189310; PubMed=9514792; DOI=10.1006/abio.1997.2558;
RA Schlieper D., Von Wilcken-Bergmann B., Schmidt M., Sobek H.,
RA Mueller-Hill B.;
RT "A positive selection vector for cloning of long polymerase chain
RT reaction fragments based on a lethal mutant of the ctp gene
RT Escherichia coli."
RL Anal. Biochem. 257:203-209(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15243036;
RA Jeong S.H., Bae I.K., Lee J.H., Sohn S.G., Kang G.H., Jeon G.J.,
RA Kim Y.H., Jeong B.C., Lee S.H.;
RT "Molecular Characterization of Extended-Spectrum Beta-Lactamases
RT Produced by Clinical Isolates of Klebsiella pneumoniae and Escherichia
RT coli from a Korean Nationwide Survey."
RL J. Clin. Microbiol. 42:2902-2906(2004).
DR EMBL; M74750; AAA24057.1; -.
DR EMBL; Y12694; CAA73226.1; -.
DR EMBL; AJ001614; CAA04868.1; -.
DR EMBL; AY425988; AAQ95605.1; -.
DR HSSP; P00807; IALO.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; plasmid; signal.
FT SIGNAL 1
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

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Query Match 100.0%; Score 1170; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.le-86;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 60
DB 24 HPEITLVKVKADBDQAGRVGTYIELDLSGKILSFPRPERPPMSTFVLLCGAVLSRID 83
QY 61 AGEOGLGRRIHYSONDLYEVSPTVEKHLTDGMTVRELCSAIIITSDNTAAILTTIGCP 120
DB 84 AGEOGLGRRIHYSONDLYEVSPTVEKHLTDGMTVRELCSAIIITSDNTAAILTTIGCP 143
QY 121 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 180
DB 144 KELTSFLNMGDHYTRLDRWPELNEAIPNDRDTMPVANAATTLRKLLTGELLTLASRQ 203
QY 181 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGERSGIIAALGPDG 228
DB 204 QLIIMWEADKVAAGPLRSALPAGWFIADKSGAGERSGIIAALGPDG 251

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RESULT 10

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084H50 PRELIMINARY; PRT; 255 AA.
ID 084H50
AC 084H50;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE TEM-117 beta-lactamase (Fragment).

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OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN
  (1)
  SEQUENCE FROM N.A.
RP Box A.T.A., Pauw A., Leverstein-vanHall M.A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130282; AAN05026.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR00871; Beta_lactamase_A.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 255
SQ SEQUENCE 255 AA; 27906 MW; DCBB28B65978C3A6 CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 255;
Best Local Similarity 99.1%; Pred. No. 2.5e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 60
DB 12 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 71
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 120
DB 72 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 191
QY 181 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 239

RESULT 11
Q84H49 PRELIMINARY; PRT; 261 AA.
AC 084H49;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE TEM-110 beta-lactamase (Fragment).
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN
  (1)
  SEQUENCE FROM N.A.
RP Box A.T.A., Pauw A., Leverstein-vanHall M.A., Verhoef J., Fluit A.C.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130283; AAN05027.1; -.
DR HSSP; Q9R435; 1HTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR00871; Beta_lactamase_A.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 28738 MW; 4F748F733A08CBB CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 261;
Best Local Similarity 99.1%; Pred. No. 2.6e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 60
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DB 12 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 71
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 120
DB 72 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 191
QY 181 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 239

RESULT 12
Q6PRU6 PRELIMINARY; PRT; 264 AA.
AC Q6PRU6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM beta-lactamase sp. U11.
OS Acinetobacter sp. U11.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=269266;
RN
  (1)
  SEQUENCE FROM N.A.
RP STRAIN=U11;
RA Ghadimi S., Hosseini-Mazinan S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583762; AAS86428.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR00871; Beta_lactamase_A.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 264
SQ SEQUENCE 264 AA; 28986 MW; A4F071CF7489352C CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 264;
Best Local Similarity 99.1%; Pred. No. 2.6e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 60
DB 12 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 71
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 120
DB 72 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 191
QY 181 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 239

RESULT 13
Q6QIV0 PRELIMINARY; PRT; 281 AA.
AC Q6QIV0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE TEM-1 beta-lactamase (Fragment).
OX NCBI_TaxID=269266;
RN
  (1)
  SEQUENCE FROM N.A.
RP STRAIN=U11;
RA Ghadimi S., Hosseini-Mazinan S.M.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY583762; AAS86428.1; -.
DR HSSP; P00807; 1ALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR00871; Beta_lactamase_A.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON_TER 1
FT NON_TER 281
SQ SEQUENCE 281 AA; 30896 MW; A4F071CF7489352C CRC64;

Query Match 99.6%; Score 1165; DB 2; Length 281;
Best Local Similarity 99.1%; Pred. No. 2.6e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 60
DB 12 HPELVKVKADADQAGRVGYIELDLSNGKILSFRRPERPFWMTGTFKVLGCVLSRD 71
QY 61 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 120
DB 72 AGQQLGRRIHYSQNDLVEYSPVTEKHLTDGVTVELCSAATWSDNTANLLTTIGSP 131
QY 121 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 180
DB 132 KELTAFILNMGDHVRRLDRWPELNEALPNDERDTTMAPAAVTTLRKLLTGELTLASRQ 191
QY 181 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 228
DB 192 QLIDMEADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDG 239

Name=blatEM-1;
```

OS *Serratia marcescens*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ES-42, ES-46, ES-71, and ES-11;
RA Yatsuyanagi J., Saito S., Harata S., Suzuki N., Amano K.-I.,
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY538700; AAS46846.1; -
DR EMBL: AY538701; AAS46847.1; -
DR EMBL: AY538702; AAS46848.1; -
DR EMBL: AY538698; AAS46844.1; -
DR HSSP; P00807; IALQ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta_lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
FT NON TER 281
SQ SEQUENCE 281 AA; 30837 MW; C8934B9C696057BF CRC64;

DR PDB; ITEM; X-ray; -
DR PDB; IXPB; X-ray; -.

Query Match 99.6%; Score 1165; DB 1; Length 286;
Best Local Similarity 99.1%; Pred. No. 2.9e-86;
Matches 226; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	HPETLVKVKQDAEDQLGARVGYI	BLDLSNGKILLESFRRPEERFP	PMSTFKVLLCGAVLSRID	60
DB	24	HPETLVKVKQDAEDQLGARVGYI	BLDLSNGKILLESFRRPEERFP	PMSTFKVLLCGAVLSRID	83
QY	61	AGQEQLGRRRIHYSQNDLVEYS	PVTEKHLTDGNTVRELCSAAIT	MSDNTAANILLTTIGP	120
DB	84	AGQEQLGRRRIHYSQNDLVEYS	PVTEKHLTDGNTVRELCSAAIT	MSDNTAANILLTTIGP	143
QY	121	KELTAFLHNMGDHYTRLDRME	PELNEAIPNDRDITMPVAMAT	TLRKLLTGELLTIASRQ	180
DB	144	KELTAFLHNMGDHYTRLDRME	PELNEAIPNDRDITMPVAMAT	TLRKLLTGELLTIASRQ	203
QY	181	QLIDMMEADKVAQPLIRSA	LPAGWFIADKSGAGERSRGI	IAALGPDG	228
DB	204	QLIDMMEADKVAQPLIRSA	LPAGWFIADKSGAGERSRGI	IAALGPDG	251

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Job time : 77.3841 secs